

Figure 1**BMV_HPP1_A**

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1 CTAGTTTACT TCTACAATTT CGGATGGAAG GATTATGGTG TAGCGTCTCT TACTACTATC 60
1 L V Y F Y N F G W K D Y G V A S L T T I 20

61 CTAGATATGG TGAAGGTGAT GACATTGACC TTACAGGAAG GAAAAGTAGC TATCCATTGT 120
21 L D M V K V M T F A L Q E G K V A I H C 40

121 CATGCAGGGC TTGGTCGAAC AGGT 144
41 H A G L G R T G 48
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BMV_HPP1_B

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1 GATGTCTTCT GGGCCCTCCT GTGGAACACA GTT 33
1 D V F W A L L W N T V 11
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Figure 2

1	GTGGCCCGGGAGGCGCCGAGGCCAGGTAGGTGCGATGGGCGTGCGAGCCCCCAACTTCTC	60
1	W P G R R R G Q V G A M G V Q P P N F S	20
61	CTGGGTGCTTCCGGGCGGCTGGCGGGACTGGCGCTGCCGCGGCTCCCCGCCCCTACCA	120
21	W V L P G R L A G L A L P R L P A H Y Q	40
121	G TTCCTGTTGGACCTGGGCGTGCGGCACCTGGTGTCCCTGACGGAGCGCGGGCCCCCTCA	180
41	F L L D L G V R H L V S L T E R G P P H	60
181	CAGCGACAGCTGCCCCGGCCTCACCCCTGCACCGCCTGCGCATCCCCGACTTCTGCCCCGC	240
61	S D S C P G L T L H R L R I P D F C P P	80
241	GGCCCCGACCAGATCGACCGCTTCGTGCAGATCGTGGACGAGGCCAACGCACGGGGAGA	300
81	A P D Q I D R F V Q I V D E A N A R G E	100
301	GGCTGTGGGAGTGCACCTGTGCTCTGGGCTTTGGCCGCACTGGCACCATGCTGGCCTGTTA	360
101	A V G V H C A L G F G R T G T M L A C Y	120
361	CCTGGTGAAGGAGCGGGGCTTGGCTGCAGGAGATGCCATTGCTGAAATCCGACGACTACG	420
121	L V K E R G L A A G D A I A E I R R L R	140
421	ACCCGGCCCCATCGAGACCTATGAGCAGGAGAAAGCAGTCTTCCAGTTCTACCAGCGAAC	480
141	P G P I E T Y E Q E K A V F Q F Y Q R T	160
481	GAAATAAGGGGCTTAGTACCCTTCTACCAGGCCCTCACTCCCCTTCCCCATGTTGTGCGA	540
161	K * G A L V P F Y Q A L T P L P H V V D	180
541	TGGGGCCAGAGATGAAGGGAAGTGGACTAAAGTATTAAACCCTCTAGCTCCCATTTGGCTG	600
181	G A R D E G K W T K V L N P L A P I G *	200
601	AAGACACTGAAGTAGCCACCCCTGCAGGCAGGTCCTGATTGAAGGGGAGGCTTGTA CTG	660
201	R H * S S P P L Q A G P D * R G G L Y C	220
661	CTTTGTTGAATAAATGAGTTTTACGAACCAGGGA AAAAAAAAAAAAAAAAAAGAAAAA	720
221	F V E * M S F T N Q G K K K K K K R K K	240
721	AAAAAAAAAAAAAAAAAAAAAAAAAGAA	746
241	K K K K K K K R	248

Figure 3

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1 ATGGCTAGAA TGAACCTCCC TGCTTCTGTG GACATTGCAT ACAAAAATGT GAGATTCTT 60
1 M A R M N L P A S V D I A Y K N V R F L 20

61 ATTACACACA ACCCAACCAA TACCTACTTT AATAGATTCT TACAGGAAC TAAAGCAGGAT 120
21 I T H N P T N T Y F N R F L Q E L K Q D 40

121 GGAGTTACCA CCATAGTAAG AGTATGAAAA GCAACTTACA ACATTGCTCT TTTAGAGAAG 180
41 G V T T I V R V * K A T Y N I A L L E K 60

181 GGAAGCATCC AGGTTCGGGA CTGGCCTTTT GATGATGGTA CAGCACCATC CAGCCAGATA 240
61 G S I Q V P D W P F D D G T A P S S Q I 80

241 ATTGATAACT GGTAAAACT TATGAAAAAT AAATTCATG AAGATCCTGG TTGTGTATT 300
81 I D N W L K L M K N K F H E D P G C C I 100

301 GCAATTCACT GTGTGTAGG TTTTGGGTGA GCTCCAGTTG CTAGTTGCCC TAGCTTTAAT 360
101 A I H C V V G F G * A P V A S C P S F N 120

361 TGAAGGTGGA ATGAAATATG AAAATGTAGT ACAGTTCATC AGATAAAAGT GACATGGAAC 420
121 * R W N E I * K C S T V H Q I K V T W N 140

421 TTTTAACAGC AAACAACCTT TGTATTGGA GAAATATTGT CTTAAATAT GCTTGCACCT 480
141 F * Q Q T T F V F G E I L S * N M L A P 160

481 CAGAAATCCC AGAAATAACT GTTCCTTCA G 511
161 Q K S Q K * L F P S 171

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Figure 4A

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1 CTCAGGCAGA ACTATGAGGC CAAGAGTGCT CATGCGCACC AGGCTTTCCT TTTGAAATTC 60
1 L R Q N Y E A K S A H A H Q A F F L K F 20

61 GAGGAGCTGA AGGAGGTGAG CAAGGAGCAG CCCAGACTGG AGGCTGAGTA CCCTGCCAAC 120
21 E E L K E V S K E Q P R L E A E Y P A N 40

121 ACCACCAAGA ACTGTAAACC ACATGTGCTA CCCTATGACC ACTCCAGGGT CAGGCTGACC 180
41 T T K N C * P H V L P Y D H S R V R L T 60

181 CAGCTGGAGG GAGAGCCTCA TTCTGACTAC ATCAATGCCA ACTTGGTCCC AGGCTACACC 240
61 Q L E G E P H S D Y I N A N L V P G Y T 80

241 CGCCACAGG AGTTCATTGC CTCTCAGGGG CCTCTCAAGA AAACACTGGA GAACTTCTGG 300
81 R P Q E F I A S Q G P L K K T L E N F W 100

301 CGGCTGGTGC GGGAGCAGCA GGTCCGCATC ATCATCATGC CGACCATCAG CATGGAGAAC 360
101 R L V R E Q Q V R I I I M P T I S M E N 120

361 GGGAGGGTGC TGTGTGAGCA TTACTGGCTG ACCGACTCTA CCCC GGACAC CCATGGTCAC 420
121 G R V L C E H Y W L T D S T P D T H G H 140

421 ATCACCATCC ACCTCCTAGC TGAGGAGCCT GAGGATGAGT GGACCAAGCG GGAATTCCAG 480
141 I T I H L L A E E P E D E W T K R E F Q 160

481 CTGCAGCAGC TTGTCCAGCA ACATCAACGG AGGGTGGAGC AACTGCAGTT CACCACCTGA 540
161 L Q H V V Q Q H Q R R V E Q L Q F T T * 180

541 TCCGACCACA GCATCCTTGA GGCTCCCAGC TCCCTGCTCG CCTTTATGGA GCTGGTACAG 600
181 S D H S I L E A P S S L L A F M E L V Q 200

601 TAGCAGGCAA GGGCCACCCA GGGCGTGGGA CCCATCCTGG TGCAGTGCAG GGGCTGTCCC 660
201 * Q A R A T Q G V G P I L V H C R G C P 220

661 TGCGGTGTGG GCATGGGCCG GACAGGCACC TTCGTGGCCC TGTCGAGGCT GCTGCAGCAG 720
221 C G V G M G R T G T F V A L S R L L Q Q 240

721 CTGGAGGAGG AGCAGATGGT AGACGTGTTT CATGCTGTGT ATGCACTCCG GATGCACCAG 780
241 L E E E Q M V D V F H A V Y A L R M H Q 260

781 CCCCTCATGA TCCAGACCTT GAGCCAGTAC GTCTTCCTGC ACAGTGCCTT ACTGAACAAG 840
261 P L M I Q T L S Q Y V F L H S C L L N K 280

841 ATTCTGGAAG GACCCCTCAA CATCTCTGAG TCTTGGCCCA TCTCTGTGAC GGACCTCCCG 900
281 I L E G P F N I S E S W P I S V T D L P 300

901 CAGGCGTGTG CCAAGAGGGC AGCCAGTGCC AATGCTGGCT TCTTGAAGGA GTACGAGGCC 960
301 Q A C A K R A A S A N A G F L K E Y E A 320

961 ATCAAGGACG AGGCTGGCTT TTCCGCACCC CCGCCTGGCT ATGAGCAGGA CAGCCCCGTC 1020
321 I K D E A G F S A P P P G Y E Q D S P V 340

1021 TCCTATGACC GTTCTCAGGG GCAGTTTCTT CCGGTGGAGG AGAGCCCCC TGACGACATG 1080
341 S Y D R S Q G Q F S P V E E S P P D D M 360

1081 CCTCTCTGGA AGCCAATGAT CTGTGCTCTG CAGGGTGGGC CCTCTGGCCG TGATCATACG 1140
361 P L W K P M I C A L Q G G P S G R D H T 380

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Figure 4B

1141 GTGCTGACTG GCCCCGCAGG GCCAAAGGAG CTCTGGGAGC TGGTGTGGCA GCACAGGGCT 1200
381 V L T G P A G P K E L W E L V W Q H R A 400

1201 CATGTGCTTG TCTCTCTTTG CCCACCCAAT GTCATGGAGA AGGAATTCTG GCCAACGGAG 1260
401 H V L V S L C P P N V M E K E F W P T E 420

1261 ATGCAGCCCC TAGTCACAGA CATGGTGACG GTGCACTGGG TGGCTGAGAG CAGCACAGCA 1320
421 M Q P V V T D M V T V H W V A E S S T A 440

1321 GGCTGTTCT GTACCCTCCT CAGGGTCACA CATGGGGAGA GCAGGAAGGA AAGGGAGGTG 1380
441 G W F C T L L R V T H G E S R K E R E V 460

1381 CAGAGACTGC AATTTCATA CCTGGAGCCT GGGCATGAGC TGCCCGCCAC CACCCTGCTG 1440
461 Q R L Q F P Y L E P G H E L P A T T L L 480

1441 CCCTTCCTGG CTGCTGTGGG CCAGTGCTGC TCTCGGGGCA ACAACAAGAA GCCGGGCACA 1500
481 P F L A A V G Q C C S R G N N K K P G T 500

1501 CTGCTCAGCC ACTCCAACAA GGGTGCAACC CAGCTGGGCA CCTTCCTGGC CATGGAGCAG 1560
501 L L S H S N K G A T Q L G T F L A M E Q 520

1561 CTGCTGCAGC AGGCAGGGTC TGAGTGCACC GTGGATATCT TTAACGTGGC CCTGCAGCAG 1620
521 L L Q Q A G S E C T V D I F N V A L Q Q 540

1621 TCTCAGGCCT GTGGCCTTAT GACCCCAACA CTGAAGCAGT ATGTCTACCT CTACACTGT 1680
541 S Q A C G L M T P T L K Q Y V Y L Y N C 560

1681 CTGAACAGCG CGCTGGCAGA CGGGCTGCCC 1710
561 L N S A L A D G L P 570

Figure 5A

1 ATGTTTCATTTTAAAAAACTTCAGGATGGGCACAAACACACAGAAGTGGGAAATGAATAAA 60
 61 AGAGTATTGATAAATTTTTGAAAATTGTTGAAGCTGAGTAATGGGCTTTCAGTCCAGTGT 120
 121 AAAGCTGTTGGAGCGCGGGAGCAAAGGTAAAGAATGATGTAATGCGCTGGCTGCTCCAAA 180
 181 GCATCTTTTGTGTGGAATGTTTATTCCAGTCATCTCTTTATGAATCAAATGTGAGGGGC 240
 241 TGCTTTGTGGACGGAGTCCTTTGCAAGAGCACATCAACGGGAAAGAGAAAGAGACATTCA 300
 301 CTTGGAGGGCTCTTGCTGAAAATGGGTTTAACTCTCCTTTTGCCAGTCACCACCAGCCTG 360
 361 ACCTCATACACTTTTAGTACAATGGAGTGGCTGAGCCTTTGAGCACACCACCATTACATC 420
 421 ATCGTGGCAAATTAAAGAAGGAGGTGGGAAAAGAGGACTTATTGTTGTCATGGCCCATGA 480
 1 M A H E 4
 481 GATGATTGGAAC TCAAATTGTTACTGAGAGGTTGGTGGCTCTGCTGGAAAGTGGAAACGGA 540
 5 M I G T Q I V T E R L V A L L E S G T E 24
 541 AAAAGTCTGCTAATTGATAGCCGCCATTTGTGGAATACAATACATCCACATTTTGGGA 600
 25 K V L L I D S R P F V E Y N T S H I L E 44
 601 AGCCATTAATATCAACTGCTCCAAGCTTATGAAGCGAAGGTTGCAACAGGACAAAGTGTT 660
 45 A I N I N C S K L M K R R L Q Q D K V L 64
 661 AATTACAGAGCTCATCCAGCATTGAGCGAAACATAAGGTTGACATTGATTGCAGTCAGAA 720
 65 I T E L I Q H S A K H K V D I D C S Q K 84
 721 GGTTGTAGTTTACGATCAAAGCTCCCAAGATGTTGCCTCTCTCTCTTCAGACTGTTTTCT 780
 85 V V V Y D Q S S Q D V A S L S S D C F L 104
 781 CACTGTACTTCTGGGTAAACTGGAGAAGAGCTTCAACTCTGTTACCTGCTTGCAGGTGG 840
 105 T V L L G K L E K S F N S V H L L A G G 124
 841 GTTTGTGAGTTCTCTCGTTGTTTCCCTGGCCTCTGTGAAGGAAAATCCACTCTAGTCCC 900
 125 F A E F S R C F P G L C E G K S T L V P 144
 901 TACCTGCATTTCTCAGCCTTGCTTACCTGTTGCCAACATTGGGCCAACCCGAATTCTTCC 960
 145 T C I S Q P C L P V A N I G P T R I L P 164

Figure 5B

961 CAATCTTTATCTTGGCTGCCAGCGAGATGTCTCAACAAGGAGCTGATGCAGCAGAATGG 1020
 165 N L Y L G C Q R D V L N K E L M Q Q N G 184

 1021 GATTGGTTATGTGTTAAATGCCAGCAATACCTGTCCAAAGCCTGACTTTATCCCCGAGTC 1080
 185 I G Y V L N A S N T C P K P D F I P E S 204

 1081 TCATTTCCTGCGTGTGCCTGTGAATGACAGCTTTTGTGAGAAAATTTGCCGTGGTTGGA 1140
 205 H F L R V P V N D S F C E K I L P W L D 224

 1141 CAAATCAGTAGATTTTCATTGAGAAAGCAAAGCCTCCAATGGATGTGTTCTAGTGCACCTG 1200
 225 K S V D F I E K A K A S N G C V L V H C 244

 1201 TTTAGCTGGGATCTCCCGCTCCGCCACCATCGCTATCGCCTACATCATGAAGAGGATGGA 1260
 245 L A G I S R S A T I A I A Y I M K R M D 264

 1261 CATGTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAGACCTACTATATCTCCAAA 1320
 265 M S L D E A Y R F V K E K R P T I S P N 284

 1321 CTTCAATTTTCTGGGCCAACTCCTGGCCTATGAGAAGAAGATTAAGAACCAGACTGGAGC 1380
 285 F N F L G Q L L A Y E K K I K N Q T G A 304

 1381 ATCAGGGCCAAAGAGCAAACCTCAAGCTGCTGCCCCTGGAGAAGCCAAATGAACCTGTCCC 1440
 305 S G P K S K L K L L P L E K P N E P V P 324

 1441 TGCTGTCTCAGAGGGTGGACAGAAAAGCGAGACGCCCTCAGTCCACCCTGTGCCGACTC 1500
 325 A V S E G G Q K S E T P L S P P C A D S 344

 1501 TGCTACCTCAGAGGCAGCAGGACAAAGGCCCGTGCATCCCGCCAGCGTGCCGAGCGTGCC 1560
 345 A T S E A A G Q R P V H P A S V P S V P 364

 1561 CAGCGTGCAGCCGTCGCTGTTAGAGGACAGCCCCTGGTACAGGCGCTCAGTGGGCTGCA 1620
 365 S V Q P S L L E D S P L V Q A L S G L H 384

 1621 CCTGTCCGCAGACAGGCTGGAAGACAGCAATAAGCTCAAGCGTTCCTTCTCTCTGGATAT 1680
 385 L S A D R L E D S N K L K R S F S L D I 404

 1681 CAAATCAGTTTCATATTCAGCCAGCATGGCAGCATCCTTACATGGCTTCTCCTCATCAGA 1740
 405 K S V S Y S A S M A A S L H G F S S S E 424

 1741 AGATGCTTTGGAATACTACAAACCTTCCACTACTCTGGATGGGACCAACAAGCTATGCCA 1800
 425 D A L E Y Y K P S T T L D G T N K L C Q 444

 1801 GTTCTCCCCTGTTTCAGGAACCTATCGGAGCAGACTCCCGAAACCAGTCCTGATAAGGAGGA 1860
 445 F S P V Q E L S E Q T P E T S P D K E E 464

Figure 5C

1861	AGCCAGCATCCCCAAGAAGCTGCAGACCGCCAGGCCCTTCAGACAGCCAGAGCAAGCGATT	1920
465	A S I P K K L Q T A R P S D S Q S K R L	484
1921	GCATTTCGGTCAGAACCCAGCAGCAGTGGCACCGCCCAGAGGTCCCTTTTATCTCCACTGCA	1980
485	H S V R T S S S G T A Q R S L L S P L H	504
1981	TCGAAGTGGGAGCGTGGAGGACAATTACCACACCAGCTTCCTTTTCGGCCTTTCCACCAG	2040
505	R S G S V E D N Y H T S F L F G L S T S	524
2041	CCAGCAGCACCTCACGAAGTCTGCTGGCCTGGGCCCTTAAGGGCTGGCACTCGGATATCTT	2100
525	Q Q H L T K S A G L G L K G W H S D I L	544
2101	GGCCCCCAGACCTCTACCCCTTCCCTGACCAGCAGCTGGTATTTTGCCACAGAGTCCTC	2160
545	A P Q T S T P S L T S S W Y F A T E S S	564
2161	ACACTTCTACTCTGCCTCAGCCATCTACGGAGGCAGTGCCAGTTACTCTGCCTACAGCTG	2220
565	H F Y S A S A I Y G G S A S Y S A Y S C	584
2221	CAGCCAGCTGCCCCTTGCGGAGACCAAGTCTATTCTGTGCGCAGGCGGCAGAAGCCAAG	2280
585	S Q L P T C G D Q V Y S V R R R Q K P S	604
2281	TGACAGAGCTGACTCGCGGCGGAGCTGGCATGAAGAGAGCCCCTTTGAAAAGCAGTTTAA	2340
605	D R A D S R R S W H E E S P F E K Q F K	624
2341	ACGCAGAAGCTGCCAAATGGAATTTGGAGAGAGCATCATGTCAGAGAACAGGTCACGGGA	2400
625	R R S C Q M E F G E S I M S E N R S R E	644
2401	AGAGCTGGGGAAAGTGGGCAGTCAGTCTAGCTTTTCGGGCAGCATGGAAATCATTGAGGT	2460
645	E L G K V G S Q S S F S G S M E I I E V	664
2461	CTCCTGAGAAGAAAGACACTTGTGACTTCTATAGACAATTTTTTTTTCTTGTTACAAAA	2520
665	S	665
2521	AAATTCCTGGGAATCTGAAATATGTATGTGGGCATACATATATATTTTTTGAAAATGGA	2580
2581	GCTATGGTGTAAAAGCAACAGGTGGATCAACCCAGTTGTTACTCTCTTAACATCTGCATT	2640
2641	TCAGAGATCAGCTAATACTTGCTCTCAACAAAAATGGAAGGGCAGATGCTAGAAATCCCCC	2700
2701	CTAGACGGAGGAAAACCATTTTATTTCAGTGAATTACACATCCTCTTGTTCTTAAAAAAGC	2760
2761	AAGTGTCTTTGGTGTGGAGGACAAAATCCCCTACCATTTTCACGTTGTGCTACTAAGAG	2820

Figure 5D

2821 ATCTCAAATATTAGTCTTTGTCCGGACCCTTCCATAGTACACCTTAGCGCTGAGACTGAG 2880
2881 CCAGCTTGGGGGTCAGGTAGGTAGACCCTGTTAGGGACAGAGCCTAGTGGTAAATCCAAG 2940
2941 AGAAATGATCCTATCCAAAGCTGATTACAAACCCACGCTCACCTGACAGCCGAGGGACA 3000
3001 CGAGCATCACTCTGCTGGACGGACCATTAGGGGCCTTGCCAAGGTCTACCTTAGAGCAAA 3060
3061 CCCAGTACCTCAGACAGGAAAGTCGGGGCTTTGACCACTACCATATCTGGTAGCCCATTT 3120
3121 TCTAGGCATTGTGAATAGGTAGGTAGCTAGTCACACTTTTCAGACCAATTCAAACCTGTCT 3180
3181 ATGCACAAAATTCCCGTGGGCCTAGATGGAGATAATTTTTTTTCTTCTCAGCTTTATGA 3240
3241 AGAGAAGGGAAACTGTCTAGGATTCAGCTGAACCACCAGGAACCTGGCAACATCACGATT 3300
3301 TAAGCTAAGGTTGGGAGGCTAACGAGTCTACCTCCCTCTTTGTAAATCAAAGAATTGTTT 3360
3361 AAAATGGGATTGTCAATCCTTTAAATAAAGATGAACTTGGTTTCAAGCCAAATGTGAATT 3420
3421 TATTTGGGTTGGTAGCAGAGCAGCAGCACCTTCAAATTCTCAGCCAAAGCAGATGTTTTT 3480
3481 GCCCTTTCTGCTTCACTGCATGGATACAGTTGGTAAATGTAATAATATGGCAGAATTTT 3540
3541 ATAGGAAACTTCCTAGGGAGGTAAATTATGGGAAGATTAAGAAAGGTACAAATTGCTGAG 3600
3601 GAGAAGCAGGAAACCTGTTTCCTTAGTGGCTTTTATCCCCTCGGCATGCGATGGGGCTGA 3660
3661 TGTTTCTATAATTGCCTCAGACTTTCACATTTACTAGTAGGGCTGAGAGAGGCTTTAGTG 3720
3721 AGGAAAGAATATTGAGAATAAAACGGTTGAGAAAGCTGAGAAGACCATTGAGTTTTGATC 3780
3781 AGTTGTGAATAGAGTGCAAAGCCATGGCCAAGCTGTTTTTGGAAACGCTGGCCGGCGTGT 3840
3841 CTTCACTGGAAAAAGCAAATCAAATGGAGCGAGAGCAAAGGGGCGTCTCAGTCCTCAA 3900
3901 CCTACAATCACTGTATGGAATCGGTCCTGGCAGCTGAACATAGGAGGTCACTGGAACAAG 3960
3961 TGATAGTGCAGATTGGCTTTCAAACATCCTCCTGGCTTGAGTTTTATCAGCTACAATGTG 4020

Figure 1. Schematic representation of the experimental design. The subjects were divided into two groups: the control group (CG) and the experimental group (EG). The CG was divided into two subgroups: the control group (CG) and the control group (CG). The EG was divided into two subgroups: the experimental group (EG) and the experimental group (EG). The subjects were divided into two groups: the control group (CG) and the experimental group (EG). The CG was divided into two subgroups: the control group (CG) and the control group (CG). The EG was divided into two subgroups: the experimental group (EG) and the experimental group (EG).

4021	GGTCCTCTTTTGAAGCCTTAATTACACAACAGCAGCTTTTGGGGGTGGGGCTGGGCGGGT	4080
4081	GTTGTCATTGTTCTTTCCCTTCCTGTAAGTGTGCTAGTTGCTGCCTCGTATCTCAGGTT	4140
4141	TTTCTCTGTTTTTGGAGAAATGGACAGTTTTTTGACCAGGATGTGACTTCATGTTTCCTAT	4200
4201	GGTGACTTCTAAAACCAGCACAGAATGATATGACTCAACACAGACCGACTTGGTTATGGG	4260
4261	GATGATGAGCCGCACAGACCTCACTAGTTGTGCACAAATAATGTGCTATGATGGGGTGTA	4320
4321	AACTGAAGGCAGAAGAGGGTCAGCCGCATTGTTATGATACTGGGAAAGTGCCGGTCAACG	4380
4381	ATTTGAGTTAGTTTTTTAGATATACATTGAAATCTTTAATCAGACATTCTCAAGTTTCACA	4440
4441	CAGTAGTTTTTGGATGTTATGTACACACACACCAAATGTGTAACAGTTCACCACTTCCAGA	4500
4501	GTGTGGTCATGCCCCAAACATGTTTAAGAAAGGAAAGCAGTAGCTCCTTGCTAACGATGT	4560
4561	TTCAGGAGGTTTGGGGCACTTGGTTTTAATGAGCTTCTGTCAATTTAGGGCTTCTCTTGGC	4620
4621	CATGGTCCCCTTCCTTCTGGAAGTGTGATGTAGTCACATCCTACAGCCTTTAGTGCTGGT	4680
4681	TCACTAGTGTGAGATAATCAGTTCTTGGAATCGAGACTGCCGTGGCGAAGGGGTGGCCTC	4740
4741	GGAGGCAGGCTCTGGAGCTGCTTGGATGTCTTTAGGTGGGGTGGTGGCTGGCTCTCTTCA	4800
4801	GCATGTAATTGGGGAAACCCTCGCGTCTACTAGGGGTGATACAGATGGTGATTTTAAAGA	4860
4861	GCAAAACTAGACTTCTATGTGAGAAGTGTCTGGAATGATTTAGGACGTGTAAAGTTAGA	4920
4921	TGGAAAGACTGTAAATGTTTAATATGAATATAGTGTTCTTTTGAAGTAAGGCCAGCTGTT	4980
4981	GAACGGTTAAACTGTGCATTTCTCATTTTGTATGTGCATGTATGTTAATGTATGAAATGA	5040
5041	TTAAATAAAATCAAACTGGTACCTGTTTATCCATAAAAAAAAAAAAAAAAAAAAAAAAAAA	5100
5101	AAAAAAAAAAG	5111

Figure 6A

		1	50
BMV_HPP1_FL	(1)	-----	
BMV_HPP1_A	(1)	-----	
BMV_HPP1_B	(1)	-----	
HS_RPTPO	(1)	MGHLPTGIHGARRLLPLLWLFLVLFKNATAFHVTVQDDNNIVVSLEASDVI	
MM_RPTPO	(1)	-----	
PYP3_SP	(1)	-----	
		51	100
BMV_HPP1_FL	(1)	-----	
BMV_HPP1_A	(1)	-----	
BMV_HPP1_B	(1)	-----	
HS_RPTPO	(51)	SPASVYVVKITGESKNYFFEFEEFNSTLPPPVIFKASYHGLYYIITLVVV	
MM_RPTPO	(1)	-----	
PYP3_SP	(1)	-----	
		101	150
BMV_HPP1_FL	(1)	-----	
BMV_HPP1_A	(1)	-----	
BMV_HPP1_B	(1)	-----	
HS_RPTPO	(101)	NGNVVTKPSRSITVLTGPLVTSVSIYDYKPSPETGVLFEIHYPEKYNVF	
MM_RPTPO	(1)	-----	
PYP3_SP	(1)	-----	
		151	200
BMV_HPP1_FL	(1)	-----	
BMV_HPP1_A	(1)	-----	
BMV_HPP1_B	(1)	-----	
HS_RPTPO	(151)	TRVNISYWEGKDFRTMLYKDFFKGKTVFNHWLPGMCYSNITFQLVSEATF	
MM_RPTPO	(1)	-----	
PYP3_SP	(1)	-----	
		201	250
BMV_HPP1_FL	(1)	-----	
BMV_HPP1_A	(1)	-----	
BMV_HPP1_B	(1)	-----	
HS_RPTPO	(201)	NKSTLVEYSGVSHEPKQHRTAPYPPQNISVRIVNLNKNWEEQSGNFPEE	
MM_RPTPO	(1)	-----	
PYP3_SP	(1)	-----	
		251	300
BMV_HPP1_FL	(1)	-----	
BMV_HPP1_A	(1)	-----	
BMV_HPP1_B	(1)	-----	
HS_RPTPO	(251)	SFMRSQDTIGKEKLFHFTEETPEIPSGNISSGWPDENSSDYETTSQPYWW	
MM_RPTPO	(1)	-----	
PYP3_SP	(1)	-----	
		301	350
BMV_HPP1_FL	(1)	-----	
BMV_HPP1_A	(1)	-----	
BMV_HPP1_B	(1)	-----	
HS_RPTPO	(301)	DSASAAPESSEDEFVSVLPMEYENNSTLSETEKSTSGSFSFFPVQMILTWL	
MM_RPTPO	(1)	-----	
PYP3_SP	(1)	-----	
		351	400
BMV_HPP1_FL	(1)	-----	
BMV_HPP1_A	(1)	-----	
BMV_HPP1_B	(1)	-----	
HS_RPTPO	(351)	PPKPPTAFDGFHIIHEREENFTEYLMVDEEAHEFVAELKEPGKYKLSVT	
MM_RPTPO	(1)	-----	
PYP3_SP	(1)	-----	

FIGURE 6B

		401		450
BMV_HPP1_FL	(1)	-----		
BMV_HPP1_A	(1)	-----		
BMV_HPP1_B	(1)	-----		
HS_RPTPO	(401)	FSSSGSCETRKSQSAKSLSFYISPSGEWIEELTEKPQHVSVHVLSTTAL		
MM_RPTPO	(1)	-----		
PYP3_SP	(1)	-----		
		451		500
BMV_HPP1_FL	(1)	-----		
BMV_HPP1_A	(1)	-----		
BMV_HPP1_B	(1)	-----		
HS_RPTPO	(451)	MSWTSSQENYNSTIVSVSLTCQKQKESQRLEKQYCTQVNSSKPIIENLV		
MM_RPTPO	(1)	-----		
PYP3_SP	(1)	-----		
		501		550
BMV_HPP1_FL	(1)	-----		
BMV_HPP1_A	(1)	-----		
BMV_HPP1_B	(1)	-----		
HS_RPTPO	(501)	PGAQYQVVIYLRKGPLIGPPSDPVTFAIVPTGIKDLMLYPLGPTAVVLSW		
MM_RPTPO	(1)	-----		
PYP3_SP	(1)	-----		
		551		600
BMV_HPP1_FL	(1)	-----		
BMV_HPP1_A	(1)	-----		
BMV_HPP1_B	(1)	-----		
HS_RPTPO	(551)	TRPYLGVERKYVVMFYFNPATMTSEWTTYEIAATVSLTASVRIANLLP		
MM_RPTPO	(1)	-----		
PYP3_SP	(1)	-----		
		601		650
BMV_HPP1_FL	(1)	-----		
BMV_HPP1_A	(1)	-----		
BMV_HPP1_B	(1)	-----		
HS_RPTPO	(601)	AWYYNFRVTMTWGDPELSCCDSSTISFITAPVAPEITSVEYFNLLYIS		
MM_RPTPO	(1)	-----		
PYP3_SP	(1)	-----		
		651		700
BMV_HPP1_FL	(1)	-----MEAGIYFNFGWKDYGVASLT-IDMVKMTTFALQEG-K		
BMV_HPP1_A	(1)	-----LVYHYNFGWKDYGVASLTILDMVKMTTFALQEGKV		
BMV_HPP1_B	(1)	-----		
HS_RPTPO	(651)	WTYGDGTTDLSHSRMLHMMVVAEGKKKIKKSVTRNVMTATISLPPGDIYN		
MM_RPTPO	(1)	-----		
PYP3_SP	(1)	-----		
		701		750
BMV_HPP1_FL	(37)	VIHCHAGLGRIGVLIAYLVFATRMTADQAIIVRAKRPNSIQTRGQLCVRE		
BMV_HPP1_A	(37)	AIHCHAGLGRIG-----		
BMV_HPP1_B	(1)	-----		
HS_RPTPO	(701)	LSVTACTERGSENTSMLRLVKLEPAPPKSLFAVNKTQTSVTLWVEEGVAD		
MM_RPTPO	(1)	-----		
PYP3_SP	(1)	-----		
		751		800
BMV_HPP1_FL	(87)	FTQFLTPLRNISCCDPKAHAVTLPQYIRQRHLLHGYEARLLHVPKIIHLV		
BMV_HPP1_A	(49)	-----		
BMV_HPP1_B	(1)	-----		
HS_RPTPO	(751)	FFEVFCCQVGSSQKTKLQEPVAVSSHVVTISSLLPATAYNCSVTSFSDHS		
MM_RPTPO	(1)	-----		
PYP3_SP	(1)	-----		

T0072 NP " 401-500"

FIGURE 6C

BMV_HPP1_FL	(137)	801	CKLLLD AENRPFMMKDVSEGPISAEIEKTMSEMTMLDKEILRHDS DVS	850
BMV_HPP1_A	(49)		-----	
BMV_HPP1_B	(1)		-----	
HS_RPTPO	(801)		PSVPTFIAVSTVTEMNPNVVVISVIAILSTLYIGILVTLILRKKHL	
MM_RPTPO	(1)		-----MYTEVNPNNVVVISVIAILSTLYIGILVTLILRKKHL	
PYP3_SP	(1)		-----	
BMV_HPP1_FL	(187)	851	PNPTAVAAEDNRCMSNEQCFDPLWKRRN---VCLQPLTHLKRRLSYS	900
BMV_HPP1_A	(49)		-----	
BMV_HPP1_B	(1)		-----	
HS_RPTPO	(851)		MARECGASTVNFASLEREGKLPYNMS-----	
MM_RPTPO	(40)		MARECGASTVNFASLEREGKLPYSWRRSVFALLTLLPSClWTDYLLAFY	
PYP3_SP	(1)		-----	
BMV_HPP1_FL	(233)	901	SDLKRAENLEQGETQTPAQILVGHKPRQKLIHCYIPQSPFPDHKEAL	950
BMV_HPP1_A	(49)		-----	
BMV_HPP1_B	(1)		-----	
HS_RPTPO	(878)		-----KNGIKKRKLINPVQLDFDAYIKDMAKSDYKFSIQFEELKLTEL	
MM_RPTPO	(90)		INPWSKNGIKKRKLINPVQLDFDSYIKDMAKSDYKFSIQFEELKLTEL	
PYP3_SP	(1)		-----MSFKEVSTENGVLTPLTITIKKAYMIIEGLNEEETEL	
BMV_HPP1_FL	(283)	951	VRSTLWFWSQKFGGLEGLKNGSPIHGRIPKEAQSCGFADVSSISPG	1000
BMV_HPP1_A	(49)		-----	
BMV_HPP1_B	(1)		-----	
HS_RPTPO	(923)		DIPHFADLPLNRCKNRYINILPYDFSRVRLVSMNEEEGADYINANKIPG	
MM_RPTPO	(140)		DIPHFADLPLNRCKNRYINILPYDFSRVRLVSMNEEEGADYINANKIPG	
PYP3_SP	(38)		LNTRLKLSKKALARNRYSNIPYENTRVRLDFMWK-EADYINASTIKI	
BMV_HPP1_FL	(333)	1001	EPVSPFANVHKDENPAHQOVHCCKTHGVGSGSVQNSRTPRSPLDGSS	1050
BMV_HPP1_A	(49)		-----	
BMV_HPP1_B	(1)		-----DVFWALWNTV-----	
HS_RPTPO	(973)		YNSPQEVYIATOGPLETRNDFWKMLQOK--SIIIVMLTQCNEKRWKCD	
MM_RPTPO	(190)		YNSPQEVYIATOGPLETRNDFWKMLQOK--SHIIVMLTQCNEKRWKCD	
PYP3_SP	(87)		P-SGKTEIATOGPTSNISIDVFWKMVWQSVPRSGIIVMLTKLRERHREKCD	
BMV_HPP1_FL	(383)	1051	KAQFLVHEHETQDSKDSSEAASHSALQSELSAARRILAAKALANLNEVEKEE	1100
BMV_HPP1_A	(49)		-----	
BMV_HPP1_B	(12)		-----	
HS_RPTPO	(1021)		HYWPFTEPIAYGDIIVEMISEE-----EQD-DWACHHER	
MM_RPTPO	(238)		HYWPFTEPIAYGDIIVEMVSEE-----EEE-DWASCHHER	
PYP3_SP	(136)		IYWFVELFETLNI GDL SVLVKVYT-----LTSLNQVQRETE	
BMV_HPP1_FL	(433)	1101	LRKVEIMWQKINSRDGAMERICGERPFILCSLMWSVWEXLEPVITKEDVD	1150
BMV_HPP1_A	(49)		-----	
BMV_HPP1_B	(12)		-----	
HS_RPTPO	(1055)		IN YADEMQDMHFNITAWPDHGVETANAESTIQFVHMVROQATKSKGPM	
MM_RPTPO	(272)		IN YADEAQDMHFNITAWPDHGVETANAESTIQFVFTVROQAASKSGPM	
PYP3_SP	(174)		INKDGVKKKILHEFYVNCWPDFGAPHTFSLISITRYIKSSSYSPDFETAPT	
BMV_HPP1_FL	(483)	1151	MLVDRAFAAEALFIEKGQHTILCVLHCIVNIQTIVDEEAFLAHAIAKAF	1200
BMV_HPP1_A	(49)		-----	
BMV_HPP1_B	(12)		-----	
HS_RPTPO	(1105)		IIHCSAGVGRGTGFALDRILQHIRDHEFVDLGLVSEMRSYRMSMNOTE	
MM_RPTPO	(322)		IIHCSAGVGRGTGFALDRILQHIRDHEFVDLGLVSEMRSYRMSMNOTE	
PYP3_SP	(224)		IIHCSAGCGRTGTGFALFEILSQTDDSTSTSKFEVDNIANIVSSLSRORM	

FIGURE 6D

		1201	1237
BMV_HPP1_FL	(533)	KVNFDSENGPTVYNTRKIFKHTLEKRRKMTDGP	KPGL
BMV_HPP1_A	(49)	-----	-----
BMV_HPP1_B	(12)	-----	-----
HS_RPTPO	(1155)	EQYIFHOCVOLMWKKKQFCISDVIYENVSKS---	---
MM_RPTPO	(372)	EQYIFHOCVOLMWKKKQFCISDVIYENVSKS---	---
PYP3_SP	(274)	QSVQSYDOLVFLYTVSQELLOGKEFLIPQL-----	-----

Figure 7A

		1	50
BMV_HPP2_FL	(1)	-----	-----
BMV_HPP2.partial	(1)	-----	-----
HS_CDC14A	(1)	-----	-----
HS_CDC14B	(1)	MKRKSERRSSWAAAPCSRRCSSTSPGVKKIRSSTQQDPRRRDPQDDVYL	
SC_CDC14	(1)	-----MRRSVYLDNTIE	
		51	100
BMV_HPP2_FL	(1)	-----	-----
BMV_HPP2.partial	(1)	-----	-----
HS_CDC14A	(1)	-MKDRLYFATLRNREKSTVNTHTFSLDEELVYENFYADFGEINLAMVYR	
HS_CDC14B	(51)	DTTDRMCFAILYSRKASASNVHYFSLDNELEYENFYADFGEINLAMVYR	
SC_CDC14	(13)	FTLRGRVYLLGAYDYTEEDTDELVEFTVEDAEFYNSFHLDFGFMNIGHTYR	
		101	150
BMV_HPP2_FL	(1)	-----	-----
BMV_HPP2.partial	(1)	-----	-----
HS_CDC14A	(50)	CCKLNKKLKSYSLSRKKIVHITCFDQKRANAATIGAVAYLYLKKTFEE	
HS_CDC14B	(101)	CCKINKKLKSITMLRKKIVHITGSDQKQANAATIGAVAYLYLGRTFEE	
SC_CDC14	(63)	AVITHEILNDPENANKAVVFSASTQRANAAACMLCCVMLVQAWTFHQ	
		151	200
BMV_HPP2_FL	(1)	-----	-----
BMV_HPP2.partial	(1)	-----	-----
HS_CDC14A	(100)	AYRAILLSGSNPPYLFFRDASRGNCYNTLLDCLQGRKGLQHCFFDFET	
HS_CDC14B	(151)	AYRILIFG-ETSYHFFRDAAAGSCNTYTLDDCFHAVKKAMQYGFLENFS	
SC_CDC14	(113)	VLQPLAQV-DPPFMPFRDAGYSNADTEITLQDVVYGVWRAKEKGLIDLHS	
		201	250
BMV_HPP2_FL	(1)	-----MGVOPPNFSWVLEGRLAGLALR-----	
BMV_HPP2.partial	(3)	GRRRGQVGAMGVOPPNFSWVLEGRLAGLALR-----	
HS_CDC14A	(150)	IDVDEYEHYERVENCDFNCIVPGKFLAFSGEHPKSKI-----ENCSPLHA	
HS_CDC14B	(200)	FNLDEYEHYERVENCDFNINIVPDRFLAFSGEHSRRL-----ESGYHQHS	
SC_CDC14	(162)	FNLDESSEYERVENCDFNVITF-DFFAFASFEQEDHPKGYLATKSSHLNQP	
		251	300
BMV_HPP2_FL	(24)	LEAHYQFLLDLQVRHLVSLTERG-PPHSDSCPGLTLHLRTPDFCFEAPD	
BMV_HPP2.partial	(35)	LEAHYQFLLDLQVRHLVSLTERG-PPHSDSCPGLTLHLRTPDFCFEAPD	
HS_CDC14A	(195)	PEAYFPYEKKHNVTAIVRLNKKIYEAKRETDACETEMDLFFIDGSTPSDN	
HS_CDC14B	(245)	PETTYQYFKNHNVTTTILNKRMYDAKRETDAGTDEHDLFFADGSTETDA	
SC_CDC14	(211)	FKSVLNFANNNVQLVRLNSHLNKKHEEDIGTQHLDLIFEDEGTCPLDS	
		301	350
BMV_HPP2_FL	(73)	QIDRFVQIVDEANARGEAVGVHCALEGRGTGTMLACYLKERCGLAGDAT	
BMV_HPP2.partial	(84)	QIDRFVQIVDEANARGEAVGVHCALEGRGTGTMLACYLKERCGLAGDAT	
HS_CDC14A	(245)	IVRRFLNICENIEG---ATAVHCKAGLGRGTGTMLACYLKHYRTHAEIT	
HS_CDC14B	(295)	IVRRFLNICENIEG---ATAVHCKAGLGRGTGTMLACYLKHYRMTAEIT	
SC_CDC14	(261)	IVKNFVCAAEITIKRGGKIAVHCKAGLGRGTCLTCAHLIYTYGETANECT	
		351	400
BMV_HPP2_FL	(123)	AEIRRLRPGSIETYEQEKAVFOFYQRTK-----	
BMV_HPP2.partial	(134)	AEIRRLRPGSIETYEQEKAVFOFYQRTKXGALVPFYQALTPLPHVVDGAR	
HS_CDC14A	(292)	AEIRICRPGSIIIGPOOH---FLEEKQSLWVQGDIERSKLKNRPSS---	
HS_CDC14B	(342)	AWRIRCRPGSVIGPOOQ---FLVMKQTNLWLEGDYERQKLGQENGQ---	
SC_CDC14	(311)	GEIRFTIRPGMVVGPOOH---WLLHLNDWFREWKYTRISLKPSEAIG---	
		401	450
BMV_HPP2_FL	(151)	-----	-----
BMV_HPP2.partial	(184)	DEGKWTQVNLPLAPLGXRHXSSPPLQAGPDXRGGLYCFVEXMSFTNQGKK	
HS_CDC14A	(335)	-EGSINKLISGLDDMSTGGNLSKTONMERFGEDNLEDDDVEMKNGITQGD	
HS_CDC14B	(386)	HRAAFSKLISGVDDTSNGVENQDQ-----QEPEPYSDDDEIN-GVTQGD	
SC_CDC14	(355)	----GLYPLISLEFYRQKKKLKDDKRVANNIEGELRDLTTPPSNGHG	

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FIGURE 7B

		451		500
BMYP_HPP2_FL	(151)	-----		
BMYP_HPP2.partial	(234)	KKKKRKKKKKKKKR-----		
HS_CDC14A	(384)	KLRALKSRQRPRTSPSCAFRRSDDTKGHPRAVSGPFRLSSSLQGS AVTLKT		
HS_CDC14B	(430)	RLRALKSRRQ-----SK-----	INAIPRLSLISREKTVLR-	
SC_CDC14	(401)	ALSARNSSQP-----	STANNCGNSFKSSAVFQTS	
		501		550
BMYP_HPP2_FL	(151)	-----		
BMYP_HPP2.partial	(249)	-----		
HS_CDC14A	(434)	SKMALSPSATAKRINRTSLSSGATVRSFSINSRLASSLGNLNAAATDDPEN		
HS_CDC14B	(460)	-----		
SC_CDC14	(430)	-----PGQPRKGQNGSNTIEDINNRRNPNTSHANR		
		551		600
BMYP_HPP2_FL	(151)	-----		
BMYP_HPP2.partial	(249)	-----		
HS_CDC14A	(484)	KKTSSSSKAGFTASPFNTLLNGSSQPTTRNYPELNNNQYNRSSNSNGNL		
HS_CDC14B	(460)	-----		
SC_CDC14	(459)	KVVIENNSDDESMQDTNGTSNHYPKVSRRKNDISSASSSRMEDNEPSAT		
		601		647
BMYP_HPP2_FL	(151)	-----		
BMYP_HPP2.partial	(249)	-----		
HS_CDC14A	(534)	NSPPGPHSAKTEEHTTILRPSYTLGLSSSSARFLRSIPSLQSEYVHY		
HS_CDC14B	(460)	-----		
SC_CDC14	(509)	NINNAADDTILROLLPKNRVTSGRRTTSAAGGIRKISGSIKK----		

[illegible]

		1		50
BMYP_HPP3	(1)	-----MARMNL	PASVDLAYKNVRF	LITNFTNTYFNRELQELKQDSVTTI
DM_PRL1	(1)	MSITMRQKDL	PAPALIEYAGMK	FLITDRESDITINHYIMELKNNVNTV
HS_PTPCAAX1	(1)	-----MARMNR	PAPVEIVTYKNMR	FLITNFTNATLNKFIEELKKYGVTTI
HS_PTPCAAX2	(1)	-----MNR	PAPVEISYENMR	FLITNFTNATLNKETEELKKYGVTTI
MM_PTPCAAX	(1)	-----MNR	PAPVEISYENMR	FLITNFTNATLNKETEELKKYGVTTI
CONSENSUS	(1)		RMNR	PAPVEISYKNMRFLITNFTNATLNKFIEELKKYGVTTI
		51		100
BMYP_HPP3	(46)	VRVXKATYNIALLEKGS	LOVPDWEFFDGTAPSS	QLIDNWLIKMKNKHEHD
DM_PRL1	(51)	VRVCEPSYNTDELETQC	ITVVKDLAFEDGTFF	PQQVDEWFEFFVLYRYQ
HS_PTPCAAX1	(46)	VRVCEATYDTTLVEKEGI	THVLDWPFDDGAPPS	NQVDDWLSVYIKKREF
HS_PTPCAAX2	(43)	VRVCDATYDKAPVEKEGI	THVLDWPFDDGAPPN	QVDDWLNLLKTKFREE
MM_PTPCAAX	(43)	VRVCDATYDKAPVEKEGI	THVLDWPFDDGAPPN	QVDDWLNLLKTKFREE
CONSENSUS	(51)	VRVCDATYD A VEKEGI	THVLDWPFDDGAPPN	QVDDWLLK KFREE
		101		150
BMYP_HPP3	(96)	--PGCCIAH	HCVVGFGXLQLL	VVALALIEGGKYNVVOFIRKXHGTFNS
DM_PRL1	(101)	QNPEACVAVHCVAGL	GRAPVLVVALALIE	LGLKYEAAVEMIRDKRRGAINA
HS_PTPCAAX1	(96)	--PGCCIAH	HCVVAGLGRAPVL	VVALALIEGGMKYEDAVQFIRQKRRGAFNS
HS_PTPCAAX2	(93)	--PGCCVAVH	HCVAGLGRAPVL	VVALALIECGMKYEDAVQFIRQKRRGAFNS
MM_PTPCAAX	(93)	--PGCCVAVH	HCVAGLGRAPVL	VVALALIECGMKYEDAVQFIRQKRRGAFNS
CONSENSUS	(101)	PGCCVAVH	HCVAGLGRAPVL	VVALALIEGMKYEDAVQFIRQKRRGAFNS
		151		180
BMYP_HPP3	(144)	KQLLYLEKYCLKTIC	HLNPRNN---	CFIIC
DM_PRL1	(151)	KQLSFL	LEKYKPKARLKHKNGHKN	--SCSVQ
HS_PTPCAAX1	(144)	KQLLYLEKYRPKMRL	RFKDSNGHRNCCIC	
HS_PTPCAAX2	(141)	KQLLYLEKYRPKMRL	RFRTDNGH	--CCVQ
MM_PTPCAAX	(141)	KQLLYLEKYRPKMRL	RFRTDNGH	---CCVQ
CONSENSUS	(151)	KQLLYLEKYRPKMRL	RFRTDNGH	CCVQ

Figure 9A

BMV_HPP4	(1)	1101	-----L R N Y E A K S A H A H Q A F	1150
MM_OST-PTP	(1101)		R R R L K G P R S E K N G F S Q E L M P Y N L W R T H R P I P H S F R Q S Y E A K S A R A H Q A F	
RN_PTP-OST	(1101)		W R C L K G P R S E K D G F S K E L M P Y N L W R T H R P I P I H S F R Q S Y E A K S A H A H Q T E	
CONSENSUS	(1101)		R L K G P R S E K G F S E L M P Y N L W R T H R P I P H S F R Q S Y E A K S A H A H Q A F	
BMV_HPP4	(17)	1151	E L K F E - L K E V S K E Q P R L E A E P A N T I T K N C X P H V L P Y D H S R V R L T Q L E G E P	1200
MM_OST-PTP	(1151)		F Q E F E E L K E V G K D Q P R L E A E P A N I T K N R Y P H V L P Y D H S R V R L T Q L S G E P	
RN_PTP-OST	(1151)		F Q E F E E L K E V G K D Q P R L E A E P D N I T K N R Y P H V L P Y D H S R V R L T Q L E G E P	
CONSENSUS	(1151)		F Q E F E E L K E V G K D Q P R L E A E H P A N I T K N R Y P H V L P Y D H S R V R L T Q L G E P	
BMV_HPP4	(66)	1201	H S D Y I N A N L M P - Y T R E Q E I A S Q G P L K K T I E N F W R L V R E Q Q V R I I M P T I	1250
MM_OST-PTP	(1201)		H S D Y I N A N F I P G Y S H P Q E I I A T Q G P L K K T L E D F W R L V W E Q Q V H V I I M L T V	
RN_PTP-OST	(1201)		H S D Y I N A N F I P G Y S H T Q E I I A T Q G P L K K T L E D F W R L V W E Q Q V H V I I M L T V	
CONSENSUS	(1201)		H S D Y I N A N F I P G Y S H P Q E I I A T Q G P L K K T L E D F W R L V W E Q Q V H V I I M L T V	
BMV_HPP4	(115)	1251	S M E N G R - L C E H Y W L T D S T P D T H G H I T I H L L A E E P E D E W T R R E F Q L Q H V - Q	1300
MM_OST-PTP	(1251)		G M E N G R V L C E H Y W F V N S T P V T H G H I T I H L L A E E S E D E W T R R E F Q L Q H G A E	
RN_PTP-OST	(1251)		G M E N G R V L C E H Y W P A N S T P V T H G H I T I H L L A E E P E D E W T R R E F Q L Q H G T E	
CONSENSUS	(1251)		G M E N G R V L C E H Y W P N S T P V T H G H I T I H L L A E E P E D E W T R R E F Q L Q H G E	
BMV_HPP4	(163)	1301	Q K Q R R V E Q L Q F T T X S D H S V P E A P S S L L A F V E L V Q E Q V A T Q G K G P I L V H C	1350
MM_OST-PTP	(1301)		Q K Q R R V E Q L Q F T T W P D H S V P E A P S S L L A F V E L V Q E Q V K A T Q G K G P I L V H C	
RN_PTP-OST	(1301)		Q K Q R R V E Q L Q F T T W P D H S V P E A P S S L L A F V E L V Q E Q V Q A T Q G K G P I L V H C	
CONSENSUS	(1301)		Q K Q R R V E Q L Q F T T W P D H S V P E A P S S L L A F V E L V Q E Q V K A T Q G K G P I L V H C	
BMV_HPP4	(213)	1351	R G C P C G V C M G R T G T F V A L S R I L Q L E E E Q V M D V E H A V Y A L R M H Q P L M I Q T	1400
MM_OST-PTP	(1351)		S ----- A G V G R T G T F V A L L P A V R Q L E E E Q V D V E N T V Y I L R L H R P L M I Q T	
RN_PTP-OST	(1351)		S ----- A G V G R T G T F V A L L R L R Q L E E E K V A D V E N T V Y I L R L H R P L M I Q T	
CONSENSUS	(1351)		S A G V G R T G T F V A L L R L L R Q L E E E Q V D V E N T V Y I L R L H R P L M I Q T	
BMV_HPP4	(263)	1401	L - Q Y F L H S C L L N K I L E G P F N I S E S W P I S V T L P Q A C A K R A A S A N A G F L K	1450
MM_OST-PTP	(1396)		L S Q Y F L H S C L L N K I L E G P S D S E S G P I P V M N F A Q A C A K R A A N A N A G F L K	
RN_PTP-OST	(1396)		L S Q Y F L H S C L L N K I L E G P D S D S E S P I S V M D F A Q A C A K R A A N A N A G F L K	
CONSENSUS	(1401)		L S Q Y I F L H S C L L N K I L E G P D A S D S G P I S V M D F A Q A C A K R A A N A N A G F L K	
BMV_HPP4	(312)	1451	E Y ----- E I K D E A G F S A P P E G Y E Q D S P S Y D R S Q G Q F S P V E E S P P D D M P L	1500
MM_OST-PTP	(1446)		E Y R L L K Q A I K D E T G S L L P P P D Y N Q N S I V S H S Q E Q F A L V E E S P A D N M I A	
RN_PTP-OST	(1446)		E Y K L L K Q A I K D G T G S L L P P P P Y N Q N S I V S R R H S Q E Q F A L V E E C P E D S M E E	
CONSENSUS	(1451)		E Y K L L K Q A I K D E T G S L L P P P D Y N Q N S I V S H S Q E Q F A L V E E S P D M L	
BMV_HPP4	(357)	1501	W K P M I C A L Q G G P S G R D H T V L T G S A G P K E L W E M V W H A H V L V S L G P P N V M	1550
MM_OST-PTP	(1496)		A S L F P ----- G G P S G R D H V L T G S A G P K E L W E M V W E H G A H V L V S L G L P D T K	
RN_PTP-OST	(1496)		A S L F P ----- G G P S G C D H V L T G S A G P K E L W E M V W E H D A H V L V S L G L P D T K	
CONSENSUS	(1501)		A S L F P G G P S G R D H V L T G S A G P K E L W E M V W E H A H V L V S L G L P D T K	
BMV_HPP4	(407)	1551	E K --- F W P T E M Q F V V T D M V T V H R V A E S - S T A G W F C T L I R V T H E S R - K E R E	1600
MM_OST-PTP	(1542)		E K P D I W P M E M Q F I V T D M V T V H R V A E S N - T A G W P S T L I R V I H G D S G K E R Q	
RN_PTP-OST	(1542)		E K P D I W P M E M Q F I V T D M V T V H R V S E S N T T T G W P S T L I R V I H G S G K E R Q	
CONSENSUS	(1551)		E K P D I W P M E M Q F I V T D M V T V H R V A E S N S T A G W P S T L I R V I H G D S G K E R Q	
BMV_HPP4	(452)	1601	V Q L Q F P H L E P G H E L P A T L L P F L A V G Q C C S R G N S K K P G T L L S H S N K G A	1650
MM_OST-PTP	(1591)		V Q L Q F P H C E T G S E L P A N T L L T F L D A V G Q C C S R G N S K K P G T L L S H S S K V T	
RN_PTP-OST	(1592)		V Q L Q F P C S E S G C E L P A N T L L T F L D A V G Q C C F R G K S K K P G T L L S H S S K N I	
CONSENSUS	(1601)		V Q L Q F P H E S G E L P A N T L L T F L D A V G Q C C S R G N S K K P G T L L S H S S K T	

Figure 9B

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      1651                                     1700
BMY_HPP4   (502) TQLSTFLAMEQLLQQAGSECTVDVFNVALQSQACGLMTPTLQYIYLYN
MM_OST-PTP (1641) NQLSTFLAMEQLLQQAGTERTVDVFNVALKQSQACGLKPTTLEQYIYLYN
RN_PTP-OST (1642) NQLSTFLAMEQLLQQAGTERTVDVFNVALKQSQACGLMTPTTLEQYIYLYN
CONSENSUS (1651) NQLGTFLAMEQLLQQAGTERTVDVFNVALKQSQACGLMTPTTLEQYIYLYN

      1701                                     1720
BMY_HPP4   (551) CLNSALADELP-----
MM_OST-PTP (1691) CLNSALRNRLPRARK-----
RN_PTP-OST (1692) CLNSALNGLPRAGKWPAPC
CONSENSUS (1701) CLNSAL NGLPRA K
```

Figure 10A

		1		50
BMY_HPP5	(1)	-MAHEMIGTQVTERLVALLESCTEKVLEIDSRPFVEYNSSHILEATNIN		
HS_DSPP8	(1)	MAGDRLPRKVMDAKKLASLLRGGPGGPLVIDSRSFVEYNSHVLSSVNIC		
MM_NPP1	(1)	MAGDRLPRKVMDAKKLASLLRGGPGGPLVIDSRSFVEYNSHVLSSVNIC		
CONSENSUS	(1)	MAGDRLPRKVMDAKKLASLLRGGPGGPLVIDSRSFVEYNS HVLSSVNIC		
		51		100
BMY_HPP5	(50)	CSKLVKRRLOQDKVLTITELIQHSAKHKVIDCSQKVVVYDQSSQDVASLS		
HS_DSPP8	(51)	CSKLVKRRLOQDKVLTITELIQPAARSQVDATEPQDVVVYDQSTRDASVLA		
MM_NPP1	(51)	CSKLVKRRLOQDKVLTITELIQPATRSQVDATEPQDVVVYDQSTRDASVLA		
CONSENSUS	(51)	CSKLVKRRLOQDKVLTITELIQPAARSQVDATEPQDVVVYDQSTRDASVLA		
		101		150
BMY_HPP5	(100)	SDCFITVLLGKLEKSNVHLLAGGFATFSSCFPGLCEGKPAALLPMSLS		
HS_DSPP8	(101)	ADSFLSILLSKLDGCFDSVAILTGGFATFSSCFPGLCEGKPAALLPMSLS		
MM_NPP1	(101)	ADSFLSILLSKLDGCFDSVAILTGGFATFSSCFPGLCEGKPAALLPMSLS		
CONSENSUS	(101)	ADSFLSILLSKLDGCFDSVAILTGGFATFSSCFPGLCEGKPAALLPMSLS		
		151		200
BMY_HPP5	(149)	QPCLPVANIGPTRILPNLYLGQKQDVLNKLMOQNGIGYVLNASNTCPKP		
HS_DSPP8	(151)	QPCLPVPSVGLTRILPHLYLGSQKQDVLNKLMTQNGISYVLNASNSCPKP		
MM_NPP1	(151)	QPCLPVPSVGLTRILPHLYLGSQKQDVLNKLMTQNGISYVLNASNSCPKP		
CONSENSUS	(151)	QPCLPVPSVGLTRILPHLYLGSQKQDVLNKLMTQNGISYVLNASNSCPKP		
		201		250
BMY_HPP5	(199)	DFICESHFTRMPVNDSECEKLLPWLDKSVDFIEKAKASNGCVVHCLAGI		
HS_DSPP8	(201)	DFICESRFRMPVINDNYCEKLLPWLDKSVDFIDKAKLSSCQVIVHCLAGI		
MM_NPP1	(201)	DFICESRFRMPVINDNYCEKLLPWLDKSVDFIDKAKLSSCQVIVHCLAGI		
CONSENSUS	(201)	DFICESRFRMPVINDNYCEKLLPWLDKSVDFIDKAKLSSCQVIVHCLAGI		
		251		300
BMY_HPP5	(249)	SRSATIAIAYIMKRMDSIDDAYRFVKLRPTISPNFNFLGQLLAYEKKI		
HS_DSPP8	(251)	SRSATIAIAYIMKTMGMSDDAYRFVKDRRPSISPNFNFLGQLLEYERTI		
MM_NPP1	(251)	SRSATIAIAYIMKTMGMSDDAYRFVKDRRPSISPNFNFLGQLLEYERSI		
CONSENSUS	(251)	SRSATIAIAYIMKTMGMSDDAYRFVKDRRPSISPNFNFLGQLLEYER L		
		301		350
BMY_HPP5	(299)	KNQTGASGPKSKLKLPLEKPNEEVAVSEGGQKSETPLSPPECADSATSE		
HS_DSPP8	(301)	KLLAALQDGP---TPSGTP---EPPSPAPAGPLP---RLPPPTSESAATG		
MM_NPP1	(301)	KLLAALQDGP---H LGTP---EPLMGPAAGIPLP---RLPPTSESAATG		
CONSENSUS	(301)	KLLAALQGD L EP P PAAG PLP RLPPPTSESAATG		
		351		400
BMY_HPP5	(349)	AAGQRP---VHPASVPSVHSVQESLLEDSPLVQALSGLHLSADRIEDSNKL		
HS_DSPP8	(344)	NAAAR---EGGLSAGGEPPAPPTPATSSALQQLRGLHLSADRIQDTNRL		
MM_NPP1	(343)	SEAATAAREGSPSAGGDAHPSAPATSSALQQLRGLHLSADRIQDTNRL		
CONSENSUS	(351)	AAAR EG SAGG PP PPT PATSALQQLRGLHLSADRIQDTNRL		
		401		450
BMY_HPP5	(397)	KRSFSLDIKSVSYASMAASLHGFSSSEDALEYKPPSTTLDGTNKLCQFS		
HS_DSPP8	(391)	KRSFSLDIKSAYAPSRRPDPGPP-----DPGEAPKLCKLD		
MM_NPP1	(393)	KRSFSLDIKSAYAPSRPDPFGPP-----DPGEAPKLCKLD		
CONSENSUS	(401)	KRSFSLDIKSAYAPSRRP PGPP DPGEAPKLCKLD		
		451		500
BMY_HPP5	(447)	PVQELSEQTPEETSPDKEEASIPKKLQTARPSDSQSKRLHSVRTSSSGTAQ		
HS_DSPP8	(427)	SPSGAALGLSSPSPDSPDAAPTAERPRRRPRP---P-----AG		
MM_NPP1	(429)	SPSGGTGLSPSPSPDSFDSVPECKRRRRRRP-----AS		
CONSENSUS	(451)	SPSG LGLSPSPSPSDA PE RPRRRR P A		
		501		550
BMY_HPP5	(497)	RSLISELHRSGS-VEDNYHTSFLGLSTSQOHLTKSAGLGLKGWHS DILA		
HS_DSPP8	(463)	SPARSPAHSLGLNFGDAARQTPRHGLSALSAPGLPGPGQAPGAWAPPL		
MM_NPP1	(464)	SPARSPAHGLGLNFGDTARQTPRHGLSALSAPGLPGPGQAPGGWVPPPL		
CONSENSUS	(501)	SPARSPAH LGLNFGD ARQTPRHGLSALSAPGLPGPGQAPGPG W PPL		

Figure 10B

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                    551                                     600
    BMY_HPP5 (546) PQTSTPSLTSSWYFATESSHFYASAIYGGASYSANSCSOLETC-----
    HS_DSPP8 (513) DSPGTSPDGPWCFSPEG-----AQGAGGVLEAPPGRAGAPGEG-----
    MM_NPP1 (514) DSPGTSPDGPWCFSPEG-----AQGPCAVFSAPGRVVSAGAPGPGNS
    CONSENSUS (551) DSPGTSPDGPWCFSPEG          A  GGGA FSAFGR  AP PG

                    601                                     650
    BMY_HPP5 (592) -----DQVYSVRRRQKPS-----DRA
    HS_DSPP8 (552) -----GGDLRRREAARA-----EPR
    MM_NPP1 (556) SSSGGGGGGGGGGGGGGGGGGSSSSSSSSSSSSSSSSSSSSSSSSSSDLRRR
    CONSENSUS (601)          GGS S RR      S          RR

                    651                                     700
    BMY_HPP5 (608) DSRRSWHHEESPFEKQFKRRSCQMEFGESEIMSENRSREELGKVGSCSFSFG
    HS_DSPP8 (568) DARTGWPEEPAPETQFKRRSCQMEFEEMVEGRARGEELAAALGKQASFSFG
    MM_NPP1 (606) DVRTGWPEEPAAADAQFKRRSCQMEFEEMVEGRARGEELAAALGKQTSFSFG
    CONSENSUS (651) D RTGWPEEPA E QFKRRSCQMEFEEMVEGRARGEELAAALGKQ SFSG

                    701
    BMY_HPP5 (658) SVEVIEVS
    HS_DSPP8 (618) SVEVIEVS
    MM_NPP1 (656) SVEVIEVS
    CONSENSUS (701) SVEVIEVS

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Figure 11

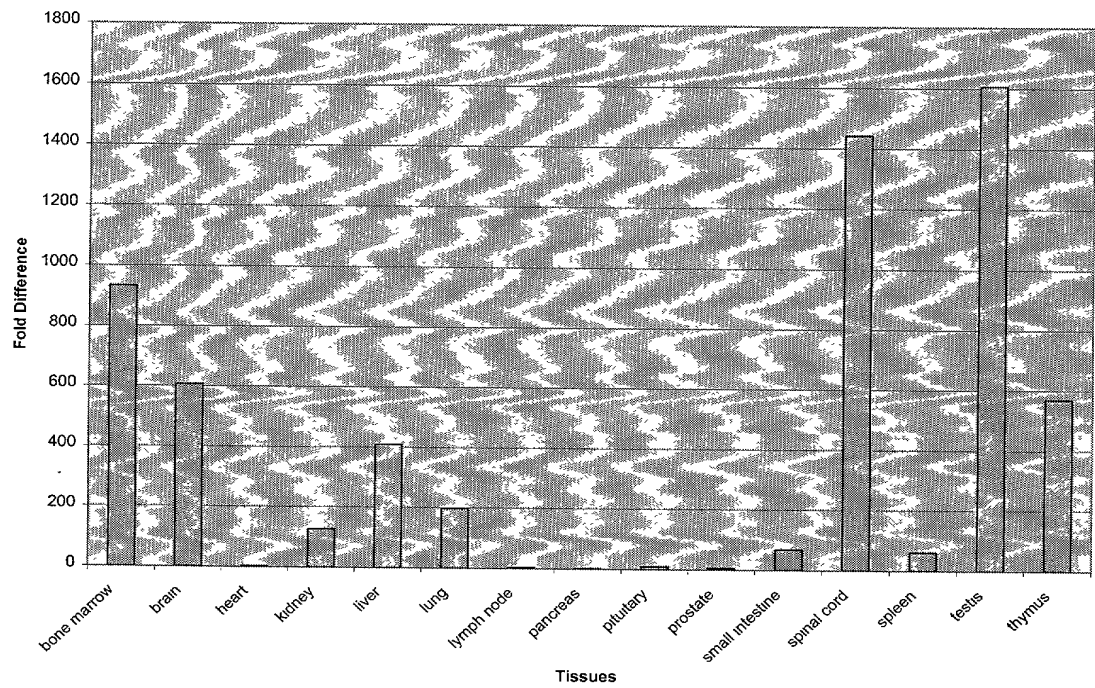


Figure 12.

BMV_HPP5

<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human dual specificity phosphatase 8	gi NP_004411	46%	58%
mouse neuronal tyrosine/threonine phosphatase 1	gi NP_032774	43%	56%

RET31

<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human protein-tyrosine phosphatase DUS8 protein	gi U27193	50.3%	56.8%
the human dual specificity MAP kinase DUSP6 protein	gi AB013382	36.5%	48.3%
human map kinase phosphatase MKP-5 protein	gi AB026436	34.3%	47.2%
mouse RET31 protein	N/A	90%	92%

mRET31

<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human protein-tyrosine phosphatase DUS8 protein	gi U27193	48.5%	55.7%
the human dual specificity MAP kinase DUSP6 protein	gi AB013382	37.4%	49.7%
human map kinase phosphatase MKP-5 protein	gi AB026436	35.2%	46.9%
human RET31 protein	N/A	90%	92%

Figure 13A

1 GAAAAGAAGACGAGGAGGAGAGCGACGGGACGGGACGCGAGCGGGAGCGCAGCCGCCCTC 60
 61 TCGGCTCCGCGGCGGCCTCGCAAGTCCGGGAGGCGAGGGGGGCCCCGAGGGGAGACGCC 120
 121 GTGACAACTTTCGTTTCCCTCTGAGGGAATTGGGAGGTCGGCGGCCCCAAAAGCTTTCAG 180
 181 TCCAGTGTAAGCTGTTGGAGCGCGGGAGCAAAGGTAAAGAATGATGTAATGCGCTGGCT 240
 241 GCTCCAAAGCATCTTTTGTGTGGAATGGTTATTCCAGTCATCTCTTTATGAATCAAATG 300
 301 TGAGGGGCTGCTTTGTGGACGGAGTCCTTTGCAAGAGCACATCAACGGGAAAGAGAAAAGA 360
 361 GACATTCACTTGGAGGGCTCTTGCTGAAAATGGGTTTAACTCTCCTTTTGCCAGTCACCA 420
 421 CCAGCCTGACCTCATACTTTTAGTACAATGGAGTGGCTGAGCCTTTGAGCACACCACC 480
 481 ATTACATCATCGTGGCAAATTAAAGAAGGAGGTGGGAAAAGAGGACTTATTGTTGTCATG 540
 1 M 1
 541 GCCCATGAGATGATTGGAAC TCAAATTGTTACTGAGAGGTTGGTGGCTCTGCTGGAAAGT 600
 2 A H E M I G T Q I V T E R L V A L L E S 21
 601 GGAACGGAAAAAGTGTGCTAATTGATAGCCGCCATTGTGGAATACAATACATCCCAC 660
 22 G T E K V L L I D S R P F V E Y N T S H 41
 661 ATTTTGAAGCCATTAATATCAACTGCTCCAAGCTTATGAAGCGAAGGTTGCAACAGGAC 720
 42 I L E A I N I N C S K L M K R R L Q Q D 61
 721 AAAGTGTTAATTACAGAGCTCATCCAGCATTGAGCGAAACATAAGGTTGACATTGATTGC 780
 62 K V L I T E L I Q H S A K H K V D I D C 81
 781 AGTCAGAAGGTTGTAGTTTACGATCAAAGCTCCCAAGATGTTGCCTCTCTCTCTTCAGAC 840
 82 S Q K V V V Y D Q S S Q D V A S L S S D 101
 841 TGTTTTCTCACTGTACTTCTGGGTAAACTGGAGAAGAGCTTCAACTCTGTTACCTGCTT 900
 102 C F L T V L L G K L E K S F N S V H L L 121
 901 GCAGGTGGGTTTGCTGAGTTCTCTCGTTGTTTCCCTGGCCTCTGTGAAGGAAAATCCACT 960
 122 A G G F A E F S R C F P G L C E G K S T 141

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Figure 13B

961 CTAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCTGTTGCCAACATTGGGCCAACCCGA 1020
 142 L V P T C I S Q P C L P V A N I G P T R 161
 1021 ATTCTTCCCAATCTTTATCTTGGCTGCCAGCGAGATGTCCTCAACAAGGAGCTGATACAG 1080
 162 I L P N L Y L G C Q R D V L N K E L I Q 181
 1081 CAGAATGGGATTGGTTATGTGTTAAATGCCAGCTATACCTGTCCAAAGCCTGACTTTATC 1140
 182 Q N G I G Y V L N A S Y T C P K P D F I 201
 1141 CCCGAGTCTCATTTCTGCGTGTGCCTGTGAATGACAGCTTTTGTGAGAAAATTTGCCG 1200
 202 P E S H F L R V P V N D S F C E K I L P 221
 1201 TGGTTGGACAAATCAGTAGATTTTATTGAGAAAGCAAAGCCTCCAATGGATGTGTTCTA 1260
 222 W L D K S V D F I E K A K A S N G C V L 241
 1261 GTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACCATCGCTATCGCCTACATCATGAAG 1320
 242 V H L A G I S R S A T I A I A Y I M K 261
 1321 AGGATGGACATGTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAGACCTACTATA 1380
 262 R M D M S L D E A Y R F V K E K R P T I 281
 1381 TCTCCAACTTCAATTTTCTGGGCCAACTCCTGGACTATGAGAAGAAGATTAAGAACCAG 1440
 282 S P N F N F L G Q L L D Y E K K I K N Q 301
 1441 ACTGGAGCATCAGGGCCAAAGAGCAAACCTCAAGCTGCTGCACCTGGAGAAGCCAAATGAA 1500
 302 T G A S G P K S K L K L L H L E K P N E 321
 1501 CCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGCGAGACGCCCTCAGTCCACCCTGT 1560
 322 P V P A V S E G G Q K S E T P L S P P C 341
 1561 GCCGACTCTGCTACCTCAGAGGCAGCAGGACAAAGGCCCGTGCATCCCGCCAGCGTGCCC 1620
 342 A D S A T S E A A G Q R P V H P A S V P 361
 1621 AGCGTGCCCGAGCGTGCAGCCGTCGCTGTTAGAGGACAGCCCGCTGGTACAGGCGCTCAGT 1680
 362 S V P S V Q P S L L E D S P L V Q A L S 381
 1681 GGGCTGCACCTGTCCGAGACAGGCTGGAAGACAGCAATAAGCTCAAGCGTTCTTCTCT 1740
 382 G L H L S A D R L E D S N K L K R S F S 401
 1741 CTGGATATCAAATCAGTTTCATATTCAGCCAGCATGGCAGCATCCTTACATGGCTTCTCC 1800
 402 L D I K S V S Y S A S M A A S L H G F S 421
 1801 TCATCAGAAGATGCTTTGGAATACTACAAACCTTCCACTACTCTGGATGGGACCAACAAG 1860
 422 S S E D A L E Y Y K P S T T L D G T N K 441

Figure 13C

1861	CTATGCCAGTTCTCCCCTGTTTCAGGAACATCGGAGCAGACTCCCGAAACCAGTCCTGAT	1920
442	L C Q F S P V Q E L S E Q T P E T S P D	461
1921	AAGGAGGAAGCCAGCATCCCCAAGAAGCTGCAGACCGCCAGGCCTTCAGACAGCCAGAGC	1980
462	K E E A S I P K K L Q T A R P S D S Q S	481
1981	AAGCGATTGCATTTCGGTCAGAACCAGCAGCAGTGGCACCAGCCAGAGGTCCCTTTTATCT	2040
482	K R L H S V R T S S S G T A Q R S L L S	501
2041	CCACTGCATCGAAGTGGGAGCGTGGAGGACAATTACCACACCAGCTTCCTTTTCGGCCTT	2100
502	P L H R S G S V E D N Y H T S F L F G L	521
2101	TCCACCAGCCAGCAGCACCTCACGAAGTCTGCTGGCCTGGGCCTTAAGGGCTGGCACTCG	2160
522	S T S Q Q H L T K S A G L G L K G W H S	541
2161	GATATCTTGGCCCCCAGACCTCTACCCCTTCCTGACCAGCAGCTGGTATTTTGCCACA	2220
542	D I L A P Q T S T P S L T S S W Y F A T	561
2221	GAGTCCTCACACTTCTACTCTGCCTCAGCCATCTACGGAGGCAGTGCCAGTTACTCTGCC	2280
562	E S S H F Y S A S A I Y G G S A S Y S A	581
2281	TACAGCTGCAGCCAGCTGCCCCACTTGCGGAGACCAAGTCTATTCTGTGCGCAGGCGGCAG	2340
582	Y S C S Q L P T C G D Q V Y S V R R R Q	601
2341	AAGCCAAGTGACAGAGCTGACTCGCGGCGGAGCTGGCATGAAGAGAGCCCCTTTGAAAAG	2400
602	K P S D R A D S R R S W H E E S P F E K	621
2401	CAGTTTAAACGCAGAAGCTGCCAAATGGAATTTGGAGAGAGCATCATGTGAGAGAACAGG	2460
622	Q F K R R S C Q M E F G E S I M S E N R	641
2461	TCACGGGAAGAGCTGGGGAAAGTGGGCAGTCAGTCTAGCTTTTCGGGCAGCATGGAAATC	2520
642	S R E E L G K V G S Q S S F S G S M E I	661
2521	ATTGAGGTCTCCTGAGAAGAAAGACACTTGTGACTTCTATAGACAATTTTTTTTTTCTTG	2580
662	I E V S	665
2581	TTCACAAAAAATCCCTGTAAATCTGAAATATATATATGTACATACATATATATTTTTG	2640
2641	GAAAATGGAGCTATGGTGTAAAAGCAACAGGTGGATCAACCCAGTTGTTACTCTCTTAAC	2700
2701	ATCTGCATTGAGAGATCAGCTAATACTTCTCTCAACAAAATGGAAGGGCAGATGCTAG	2760
2761	AATCCCCCTAGACGGAGGAAAACATTTTATTTCAGTGAATTACACATCCTCTTGTCTT	2820

[illegible][illegible]

Figure 13E

3961 GTCCTCAACCTACAATCACTGTATGGAATCGGTCCTGGCAGCTGAACATAGGAGGTCACT 4020
 4021 GGAACAAGTGATAGTGCAGATTGGCTTTCAAACATCCTCCTGGCTTGAGTTTTATCAGCT 4080
 4081 ACAATGTGGGTCCTCTTTTGAAGCCTTAATTCACAACAGCAGCTTTTTGGGGGTGGGGCT 4140
 4141 GGGCGGGTGTTGTCATTGTTCTTTCCCTTCCTGTAAGTGTCGCTAGTTGCTGCCTCGTAT 4200
 4201 CTCAGGTTTTTCTCTGTTTTTGAGAAATGGACAGTTTTTTGACCAGGATGTGACTTCATG 4260
 4261 TTTCTATGGTGACTTCTAAAACCAGCACAGAATGATATGACTCAACACAGACCGACTTG 4320
 4321 GTTATGGGGATGATGAGCCGCACAGACCTCACTAGTTGTGCACAAATAATGTGCTATGAT 4380
 4381 GGGGTGTAAAGTGAAGGCAGAAGAGGGTCAGCCGCATTGTTATGATACTGGGAAAGTGCT 4440
 4441 GGTCAACGATTTGAGTTAGTTTTTTAGATATACATTGAAATCTTTAATCAGACATTCTCAA 4500
 4501 GTTTCACACAGTAGTTTTTGATGTTATGTACACACACACCAAATGTGTAACAGTTCACCA 4560
 4561 CTTCCAGAGTGTGGTCATGCCCAAAACATGTTTAAGAAAGGAAAGCAGTAGCTCCTTGCT 4620
 4621 AACGATGTTTCAGGAGGTTTGGGGCACTTGTTTTAATGAGCTTCTGTCATTTAGGGCTT 4680
 4681 CTCTTGGCCATGGTCCCTTCTTCTGGAACGTGATGTAGTCACATCCTACAGCCTTTA 4740
 4741 GTGCTGGTTCACTAGTGTGAGATAATCAGTTCTTGGAATCGAGACTGCCGTGGCGAAGGG 4800
 4801 GTGGCCTCGGAGGCAGGCTCTGGAGCTGCTTGATGTCTTTAGGTGGGGTGGTGGCTGGC 4860
 4861 TCTCTTCAGCATGTAATTGGGGAAACCCTCGCGTCTACTAGGGGTGATACAGATGGTGAT 4920
 4921 TTAAAGAGCAAACTAGACTTCTATGTGAGAAGTGCTGGAAAATGATTTAGGACATGTG 4980
 4981 TAAAGTTAGATGGAAAGACTGTAAATGTTAATATGAATATAGTGTTCTTTTGAAGTAAG 5040
 5041 GCCAGCTGTTGAACGGTTAACTGTGCATTTCTCATTTTGATGTGTCATGTATGTTAATG 5100
 5101 TATGAAATGATTAAATAAAATCAAACTGGTACCTGTTTATACATAAATACGAGAAAAGA 5160

Figure 13F

5161 CCTATCTTTGCAGCCATAAACTCGGTGGGAACACCACCACTCAAGTTGCCAAAGGAGGCA 5220
5221 GTGGTGAAACCTGTCTCTGTTCTCACTTAAATGAGGATTTAGCTCAAAATAAAGTGGTGGT 5280
5281 GTCATCAGGTTTATTCCGTGTTCTGTCAATTCACATGGAACACCGGATGATTAGCTAACAG 5340
5341 TTTAGTGCCAGCCTTCATTCTTTACTGTGTACGTTAAATGCACACTACAGTGAAAAAGCC 5400
5401 TAAGACACTTGGTAAATATTTTCTAGCTGACTGATTCCAGAACACACAAG 5450

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Figure 14A

		1	50
RET31	(1)	-----	-----
mRET31	(1)	-----	-----
DUS6	(1)	-----	-----
DUS8	(1)	-----	-----
MKP-5	(1)	MPPSPLDLDRVVVALSRPVRPQDLNLCLDSSYLGSANPGSNSHPPVIATT	
		51	100
RET31	(1)	-----	-----
mRET31	(1)	-----	-----
DUS6	(1)	-----	-----
DUS8	(1)	-----	-----
MKP-5	(51)	VSLKAANLTYMPSSSGSARSNLNCGCSSASCCTVATYDKDNQAQTQAI AAG	
		101	150
RET31	(1)	-----MAHEMIGTQIVTERLVALLESCT-----	-----
mRET31	(1)	-----MAHEMIGTQIVTESLVALLESCT-----	-----
DUS6	(1)	-----MIDTLRPVPFASEMIAISKTVAWLNQLELCN-----	-----
DUS8	(1)	-----MAGDRIPRKVMDAKKLASLIRGGP-----	-----
MKP-5	(101)	TTTTAIGTSTTCPANQMNNNNENTGSLSPSSGVGSPVSGTPKQLASIKII	
		151	200
RET31	(24)	-----EKVLLIDSRPFVEYNTSHILEAININCSKLM-----	-----
mRET31	(24)	-----EKVLLIDSRPFVEYNTSHILEAININCSKLM-----	-----
DUS6	(32)	-----ERLLMDCRPQELYESSHIESAINVAIPGIM-----	-----
DUS8	(25)	-----GGPLMIDSRPFVEYNSWHVLSVNICCSKLM-----	-----
MKP-5	(151)	YPNDLAKKMTKCSKSHLPSGGPVLLIDCRPFMEYNKSHIQGAVHINCADKI	
		201	250
RET31	(55)	KRRLOQD--KVITELIQHSKHKVIDCSORVVVYDQSS--QDVASLSSD	
mRET31	(55)	KRRLOQD--KVITELIQHSKHKVIDCNORVVVYDHSS--QDVGSLSSD	
DUS6	(63)	LRRLOKGNLPVRALEFTRGETRDRFTTRCGTDTVVLYDESSSDWNENTGCF	
DUS8	(56)	KRRLOQG--KVIAELIQPAARSOVATEPQDVVYDQST--RDASVLAAD	
MKP-5	(201)	SRRRLQGGKITVLDLISCREGKDSFKRIFSKETVYDENTNEPSRVMPFSQ	
		251	300
RET31	(102)	CFLTIVLLGKLENSFNSVHLLAGGFABFSRCFPGLCEGK-STLVPPTCISQP	
mRET31	(102)	CFLTIVLLGKLRSFNSVHLLAGGFABFSRCFPGLCEGK-STLVPPTCISQP	
DUS6	(113)	SLIGILLKKLKDEGCRAFYLEGGFSEKQAEFSLHCETN--LDGSCSSSSP	
DUS8	(103)	SFLSILLSKLDGCFDSVAILLTGGFATFSSCFPGLCEGKPAALLPMSISQP	
MKP-5	(251)	-PLHIVLESLEKREGKEPLVILKGLSSEKQNIENLQDNLQLOQECREVGGG	
		301	350
RET31	(151)	CLPVANIG-----PTRI	
mRET31	(151)	CLPVANIG-----PTRI	
DUS6	(161)	PLPVLGLGLRISDSSSDIESDLDRDPNSATDSDGSPLSNSQPSFPVETI	
DUS8	(153)	CLPVPSVG-----LTRI	
MKP-5	(300)	ASAASSLLPQPIPTTPDIEN-----AELTPI	
		351	400
RET31	(163)	LPNLYLGCAQDVLNKLQOONGIGYVLNASYTCP-KPDFIPESHFLRVPV	
mRET31	(163)	LPNLYLGCAQDVLNKDLMOONGIGYVLNASNTCP-KPDFIPESHFLRVPV	
DUS6	(211)	LPFLYLGCARDSTNLVLEFGIKYLLNMVPLPLNLFNAGEFKYKQPTI	
DUS8	(165)	LPFLYLGCARDVLNKLDMTONGISYVLNASNSCP-KPDFICESRFMRVPI	
MKP-5	(326)	LPFLFLCNEQDAQDLDTMOGLNIGYVINVTTHLPLYHYEKGFLFNKRI PA	

40072 NP

Figure 14B

```

401                                     450
RET31 (212) NDSFCEKILPWLDKSVDFIEKAKASNGCVLVHCLAGISRSATIAIAYIMK
mRET31 (212) NDSFCEKILPWLDKSVDFIEKAKASNGCVLIHCLAGISRSATIAIAYIMK
DUS6 (261) SDHWSONLSQTPPEAISFIDEARGKNCGLVHCLAGISRSITVTVAYIMQ
DUS8 (214) NDNYCEKLLPWLDKSLDFIDKAKLSSCOVIVHCLAGISRSATIAIAYIMK
MKP-5 (376) TDSNKNQNTROYFEELAFEFIEFAHQCKGLLHCOAGVRSATITVAYIMK

451                                     500
RET31 (262) RMDMSLDEAYRFVKEKRPTISPNNFNFLGQLLDYEKKTKNOTGASGPKSKL
mRET31 (262) RMDMSLDEAYRFVKEKRPTISPNNFNFMGQLLDYEKTINNOTGMSGPKSKL
DUS6 (311) KLINISNDAYDITVKMKKSNISPNNFNFMGQLLDYEFTLGLSSPCDNRVPAQ
DUS8 (264) TGMSSDDAYRFVKDRRPSISPNNFNFLGQLLEYERTLKLLAALQCDPG--
MKP-5 (426) PTRMTMTDAYKFKVKCRPTISPNNFNFMGQLLEYEDINNGWTPRILTPKL

501                                     550
RET31 (312) KLHLHLEKPNEPVPVAVSEGGQKSETPLSPPCADSATSEAGQRP--VHPAS
mRET31 (312) KLHLHLDKPSEPVPFAASEGGWKSALSLSPPCAN-STSEASGQRL--VHPAS
DUS6 (361) QLYFTTPSNQNVYQVSLQST-----
DUS8 (312) -TPSG----TPEPPPSPAAGAPLPRLPPTSESAAAGNAAAREGGISAQG
MKP-5 (476) MGVETVV-----

551                                     600
RET31 (360) VPSVPSVQPSLLEDSPILVOALSGLHLSADRLLEDENKLRFSFLDIKSVSY
mRET31 (359) VE---RLQPSLLEDSPILVOALSGLQLSSEKLEDSKLRFSFLDIKSVSY
DUS6 (382) -----
DUS8 (357) EE---PAPETIPPATSAEQGLRGLHLSADRLQDINRLKRSFSLDIKSA-Y
MKP-5 (483) -----

601                                     650
RET31 (410) SASMAASLHGFSSSEDALEYKPKSTTLDGTNKLQCFSPVQEVSEQSPETS
mRET31 (406) SASMAASLHGFSS-EEALDYCKPSATLDGTNKLQCFSPVQEVSEQSPETS
DUS6 (382) -----
DUS8 (403) APSRRPDGPGPPDPGEAPKLCKLDSPSG-----AALGSSPSSE-DS
MKP-5 (483) -----

651                                     700
RET31 (460) PDKEEASIPKKLQTAAPSDDSQSKRLHSVRTSSSGTAQRSLLSPLHRSQS-
mRET31 (455) PDKEEAHIPKQPPRPSESQVTRLHSVRTGSSGSTQRPFFSPLHRSQS-
DUS6 (382) -----
DUS8 (443) PDAAPEARPPRRRRPP-----AGSPARSPAHSLGLN
MKP-5 (483) -----

701                                     750
RET31 (509) VEDNYHTSFLFGLSTSQQHLTKSAG--LCLKGWHSDTLAPQTSTPSLTSS
mRET31 (504) VEDNYHTNFLFGLSTSQQHLTKSAG--LCLKGWHSDTLAPQSSAPSLTSS
DUS6 (382) -----
DUS8 (476) FGDAARQTPRHGLSALSAPGLPGPCQFACPGAWAPPIDSE--GTSPDPGP
MKP-5 (483) -----

751                                     800
RET31 (557) WYFATESSHFYASAIYGCASYSASCSQLPTCGDQVYSVRRRQKPSDR
mRET31 (552) WYFATEPSHLYSASAIYGCNSSYSASCSQLPTCSDQIYSVRRRQKPTDR
DUS6 (382) -----
DUS8 (524) WCFSPE-----GAQCAGGVLEAPFGRAGAPGPGGGSDLRRREAARAP
MKP-5 (483) -----

```

Figure 14C

		801		850
RET31	(607)	ADSRRSWHEESPFEKQFKRRSCQMEFGESIMSENRSREELGKMGSSFS		
mRET31	(602)	ADSRRSWHEESPFEKQFKRRSCQMEFGESIMSENRSREELGKMGSSFS		
DUS6	(382)	-----		
DUS8	(567)	RDARTGWPEEPAPETQFKRRSCQMEFEGMVEGRARGEELAAIGKSSFS		
MKP-5	(483)	-----		
		851		
RET31	(657)	GSMEIEVS		
mRET31	(652)	GSMEIEVS		
DUS6	(382)	-----		
DUS8	(617)	GSMEIEVS		
MKP-5	(483)	-----		

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Figure 15.

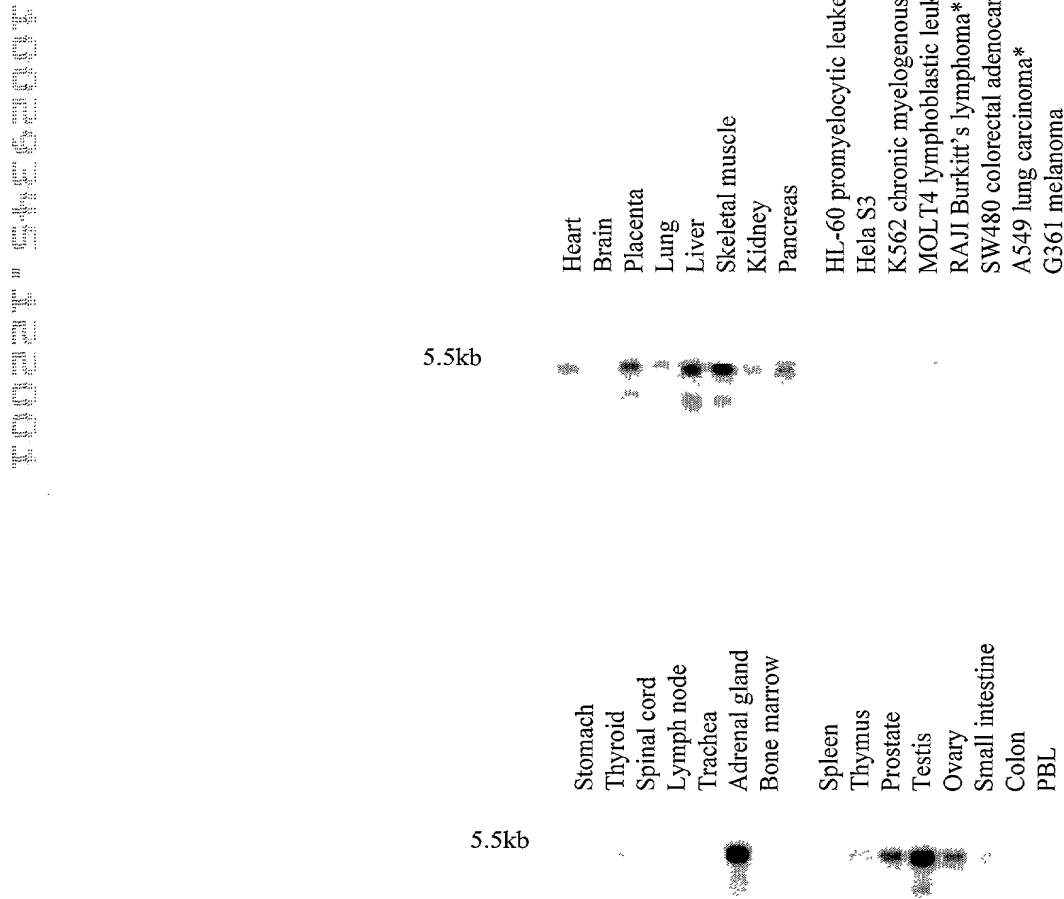


Figure 16A

1 GACTGAGGTTGTGAGCCAGTGTAAAGCTGTTGGAGTGAGGGCAGAAAGGTAAAGGATGA 60
 61 TGTAATGCCTGGCTGCCCTAGAGCATCTTTTGTGTGGGATGGGTATTCCCATCATCTCT 120
 121 ATGAATCTAGTGTGAGGGGCTGCTTTGTGGAAGGAATCCTTTGCAAGAGCATATCAACAG 180
 181 GAAAGAGAAAGAGACATTGAGTTGGAGGGCTCTTGCTGAAATGGATTAACTCTCCTCTT 240
 241 GCCAGTCACCACTAGCCTGACCTCATACTTTTGTAGTACAATGGAGTGGCTGAGCCTTTG 300
 301 AGCACAGCACCATTACATCATCGTGGCAAATTAAAGAACGAGGTGGGGAAAGAGGACTTA 360
 361 TTGTTGTCATGGCCCATGAGATGATTGGAAGTCAAATTGTTACTGAGAGCTTGGTGGCTC 420
 1 M A H E M I G T Q I V T E S L V A L 18
 421 TGCTGGAAGTGAACGGAAAAAGTGCTGCTAATTGATAGCCGACCATTGTGGAATACA 480
 19 L E S G T E K V L L I D S R P F V E Y N 38
 481 ATACGTCTCACATTTTGAAGCCATTAATATCAACTGCTCCAACTGATGAAGCGAAGGT 540
 39 T S H I L E A I N I N C S K L M K R R L 58
 541 TGCAACAGGACAAAGTATTAATTACAGAACTAATCCACCAATCTACAAAGCATAAGGTTG 600
 59 Q Q D K V L I T E L I H Q S T K H K V D 78
 601 ACATTGACTGCAATCAAAGAGTGGTAGTTTATGATCACAGTTCACAAGATGTTGGTTCTC 660
 79 I D C N Q R V V V Y D H S S Q D V G S L 98
 661 TGTCGTCAGACTGCTTTCTCACTGTACTTCTGGGTAAGCTGGAGAGAAGCTTCAACTCTG 720
 99 S S D C F L T V L L G K L E R S F N S V 118
 721 TCCACCTGCTTGAGGTGGCTTTGCTGAGTTCTCTCGTTGTTTCCCTGGCCTCTGTGAAG 780
 119 H L L A G G F A E F S R C F P G L C E G 138
 781 GAAAGTCCACTCTAGTCCCTACCTGCATATCTCAGCCTTGCTTACCTGTTGCGAACATTG 840
 139 K S T L V P T C I S Q P C L P V A N I G 158
 841 GGCCAACTCGAATTCTTCCAATCTCTATCTTGGCTGCCAGCGAGATGTCTCAACAAGG 900
 159 P T R I L P N L Y L G C Q R D V L N K D 178
 901 ACCTGATGCAACAGAATGGGATTGGCTATGTGTTAAATGCCAGCAATACCTGTCCAAAGC 960
 179 L M Q Q N G I G Y V L N A S N T C P K P 198

Figure 16B

961	CTGACTTCATACCTGAATCTCACTTCCTGCGAGTGCCTGTGAATGACAGCTTTTGTGAGA	1020
199	<u>D F I P E S H F L R V P V N D S F C E K</u>	218
1021	AAATCCTACCATGGTTGGACAAGTCTGTGGATTTTCATTGAGAAAGCAAAAGCCTCCAATG	1080
219	<u>I L P W L D K S V D F I E K A K A S N G</u>	238
1081	GCTGTGTGCTTATCCACTGCTTAGCTGGGATCTCTCGCTCCGCCACTATTGCTATTGCCT	1140
239	<u>C V L I H C L A G I S R S A T I A I A Y</u>	258
1141	ACATCATGAAGAGGATGGACATGTCTCTAGATGAGGCTTACAGATTTGTGAAAGAAAAAA	1200
259	<u>I M K R M D M S L D E A Y R F V K E K R</u>	278
1201	GACCTACTATATCTCCGAATTTTAATTTTATGGGCCAACTCATGGACTATGAGAAGACGA	1260
279	<u>P T I S P N F N F M G Q L M D Y E K T I</u>	298
1261	TTAATAACCAGACTGGAATGTCAGGGCCAAAGAGCAAAGCTGAAGCTGCTGCACCTAGACA	1320
299	N N Q T G M S G P K S K L K L L H L D K	318
1321	AACCCAGTGAGCCCGTGCCTGCAGCCTCAGAGGGCGGATGGAAGAGTGCACCTGTCTCTCA	1380
319	P S E P V P A A S E G G W K S A L S L S	338
1381	GTCCACCCTGTGCCAACTCGACCTCGGAGGCATCAGGGCAAAGGCTTGTGCATCCTGCAA	1440
339	P P C A N S T S E A S G Q R L V H P A S	358
1441	GTGTGCCCCGCTTACAGCCGTCACTCTTAGAGGACAGTCCGCTGGTACAGGCGCTCAGTG	1500
359	V P R L Q P S L L E D S P L V Q A L S G	378
1501	GGCTCCAGCTGTCTCTCAGAGAAGCTGGAAGACAGCACTAAGCTCAAGCGTTCCTTCTCTC	1560
379	L Q L S S E K L E D S T K L K R S F S L	398
1561	TCGATATCAAATCTGTTTCATATTAGCCAGTATGGCCGCTCCCTACACGGCTTCTCGT	1620
399	D I K S V S Y S A S M A A S L H G F S S	418
1621	CAGAGGAGGCTTTAGACTACTGCAAACCTTCTGCCACACTGGATGGGACCAACAAGCTCT	1680
419	E E A L D Y C K P S A T L D G T N K L C	438
1681	GCCAGTTCTCCCCCGTTTTCAGGAGGTATCAGAACAGAGTCCAGAGACCAGCCCGGATAAGG	1740
439	Q F S P V Q E V S E Q S P E T S P D K E	458
1741	AGGAGGCCACATCCCCAAGCAGCCCCAACCTCCCAGGCCTTCTGAGAGCCAGGTCACAC	1800
459	E A H I P K Q P Q P P R P S E S Q V T R	478
1801	GCTTGCACTCAGTGAGAACCGGCAGTAGTGGGTCCACCCAGAGGCCCTTCTTCTCGCCAC	1860
479	L H S V R T G S S G S T Q R P F F S P L	498

Figure 16C

1861 TGCATCGGAGCGGGAGTGTAGAGGACAATTACCATACCAACTTCCTTTTTGGCCTTTCCA 1920
 499 H R S G S V E D N Y H T N F L F G L S T 518
 1921 CCAGCCAGCAACACCTCACCAAGTCTGCAGGGCTTGGCCTCAAGGGCTGGCACTCAGATA 1980
 519 S Q Q H L T K S A G L G L K G W H S D I 538
 1981 TTCTGGCTCCCCAGTCCTCTGCCCCCTCCCTGACCAGCAGTTGGTATTTTGCTACGGAGC 2040
 539 L A P Q S S A P S L T S S W Y F A T E P 558
 2041 CTTCACTTGTACTCTGCTTCAGCCATCTATGGAGGCAACAGCAGTTACTCTGCCTACA 2100
 559 S H L Y S A S A I Y G G N S S Y S A Y S 578
 2101 GCTGTGGCCAGCTGCCCCACTTGCACTGACCAAATCTATTCTGTTCGTAGGCGGCAGAAGC 2160
 579 C G Q L P T C S D Q I Y S V R R R Q K P 598
 2161 CTACTGACAGAGCTGACTCGAGGCGGAGCTGGCATGAAGAGAGCCCCCTTTGAAAAGCAGT 2220
 599 T D R A D S R R S W H E E S P F E K Q F 618
 2221 TTAAACGCAGAAGCTGCCAATGGAATTTGGAGAGAGCATTATGTCGGAGAACAGGTCCA 2280
 619 K R R S C Q M E F G E S I M S E N R S R 638
 2281 GGGAGGAGCTGGGCAAGGTGGGCAGCCAGTCCAGCTTCTCCGGCAGCATGGAGATCATCG 2340
 639 E E L G K V G S Q S S F S G S M E I I E 658
 2341 AGGTCTCTTGAGAAGACCTCGTCGCTTCTGTTGACAGTTTGTTCCTGTTTACAAAAA 2400
 659 V S 660
 2401 TAGTCCCTGTAAATCTGAAATATGTATATGTACATACATATATATTTTTGGAATATAGAG 2460
 2461 CTACGGTATAAAAGCAACAGATGGATCAACACAGTTGTTCTCTCAGCACCTGCACTGAGA 2520
 2521 ATAGCTAACTCTCAGAAAAGATTGGAAGGGTAGATGTTAGAATTCTCCCAGCCAGGAGAA 2580
 2581 GAGATTTGGTTCAGTGAATTGCACATCTTCTGTTCTACAAAAGCAAGGGTTTTGTTTG 2640
 2641 TTTGTATGTTGTTGTTTTAATGTTAGAGGGCAAATCCCTCCCATTTTCACGTGCAAC 2700
 2701 AGAGGTCTCAGAACTCATCTCTGTCCAGGCCCTTCCCTAGTGCACCTTAGCGCTAA 2756

Figure 17.

Ret31_DSPc G P T R L P N Y L C Q R D V L N K E L M Q Q N G G V L N A S Y T C K P D F I P E S H F
DUS8_DSPc G L T R L P H Y L S Q K D V L N K D L M T Q N G S Y V L N A S N S C P K P D F I C E S R F
MKP5_DSPc E L T P L P F L F L S N E Q D A Q D L D T M Q R L N G Y V I N V T T H L P L Y H Y E K G L F N Y
DUS6_DSPc F P V E L P F L Y L G C A K D S T N L D V L E E F G K Y I L N V T P N L P N L F E N A G E F K Y

Ret31_DSPc L R V V N S F C E K I L P W L D K S V D E K A K A S N G C V L V H O L A G I S R S A T I A I
DUS8_DSPc M R V I N D N Y C E K I L P W L D K S I E F D K A K L S S C Q V I V H O L A G I S R S A T I A I
DUS6_DSPc K Q I I S D H W S Q N I S Q F F E A I S F I D E A R G K N C G V L V H O L A G I S R S V T V T V
MKP5_DSPc K R L A T D S N K Q N L R Q Y F E E A F E F E E A H Q C G K G L L I H Q Q A C V S R S A T I V I

Ret31_DSPc I K R M D M S L D E A Y R F V A E K R P T S P N F N F L C O L D Y K K
DUS8_DSPc A Y I M K T M G M S S D A Y R F V K D R R P S S P N F N F L C O L E Y E R T
MKP5_DSPc A Y L M K H T R M I M T A Y K F V G K R P I S P N L N F M C O L E F E E D
DUS6_DSPc A Y L M Q K L N L S M N D A Y D I V K M K S N S P N F N F M C O L E D F E R T

Figure 18

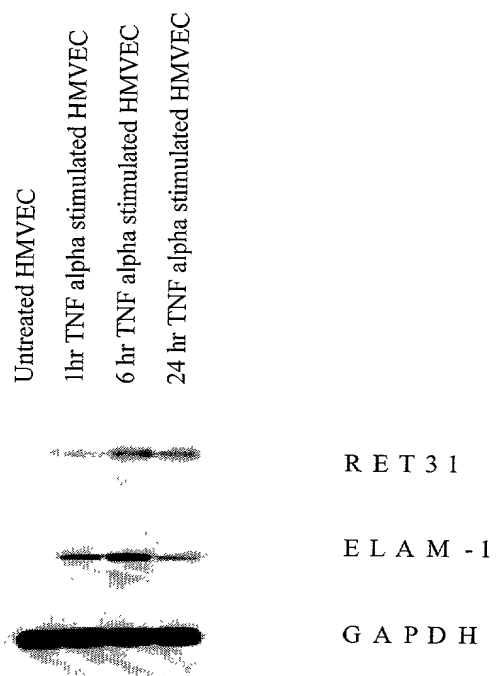


Figure 19A

1 GAAAAGAAGACGAGGAGGAGAGCGACGGGACGGGACGCGAGCGGGAGCGCAGCCGCCCTC 60
 61 TCGGCTCCGCGGCGGCGCCTCGCAAGTCCGGGAGGCGAGGGGGGCCCCGAGGGGAGACGCC 120
 121 GTGACAACTTTCGTTTCCCTCTGAGGGAATTGGGAGGTCGGCGGCCCCAAAAGCTTTCAG 180
 181 TCCAGTGTAAGCTGTTGGAGCGCGGGAGCAAAGGTAAAGAATGATGTAATGCGCTGGCT 240
 241 GCTCCAAAGCATCTTTTGTGTGGAATGGTTATTCCAGTCATCTCTTTATGAATCAAATG 300
 301 TGAGGGGCTGCTTTGTGGACGGAGTCCTTTGCAAGAGCACATCAACGGGAAAGAGAAAAGA 360
 361 GACATTCACTTGGAGGGCTCTTGCTGAAAATGGGTTTAACTCTCCTTTTGCCAGTCACCA 420
 421 CCAGCCTGACCTCATACTTTTAGTACAATGGAGTGGCTGAGCCTTTGAGCACACCACC 480
 481 ATTACATCATCGTGGCAAATTAAGAAGGAGGTGGGAAAAGAGGACTTATTGTTGTCATG 540
 1 M 1
 541 GCCCATGAGATGATTGGAAC TCAAATTGTTACTGAGAGGTTGGTGGCTCTGCTGGAAAGT 600
 2 A H E M I G T Q I V T E R L V A L L E S 21
 601 GGAACGGAAAAAGTGCTGCTAATTGATAGCCGCCATTTGTGGAATACAATACATCCCAC 660
 22 G T E K V L L I D S R P F V E Y N T S H 41
 661 ATTTTGAAGCCATTAATATCAACTGCTCCAAGCTTATGAAGCGAAGGTTGCAACAGGAC 720
 42 I L E A I N I N C S K L M K R R L Q Q D 61
 721 AAAGTGTTAATTACAGAGCTCATCCAGCATTGAGCGAAACATAAGGTTGACATTGATTGC 780
 62 K V L I T E L I Q H S A K H K V D I D C 81
 781 AGTCAGAAGGTTGTAGTTTACGATCAAAGCTCCCAAGATGTTGCCTCTCTCTCTTCAGAC 840
 82 S Q K V V V Y D Q S S Q D V A S L S S D 101
 841 TGTTTTCTCACTGTACTTCTGGGTAAACTGGAGAAGAGCTTCAACTCTGTTCACCTGCTT 900
 102 C F L T V L L G K L E K S F N S V H L L 121
 901 GCAGGTGGGTTTGCTGAGTTCTCTCGTTGTTTCCCTGGCCTCTGTGAAGGAAAATCCACT 960
 122 A G G F A E F S R C F P G L C E G K S T 141

Figure 19B

961	CTAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCTGTTGCCAACATTGGGCCAACCCGA	1020
142	L V P T C I S Q P C L P V A N I G P T R	161
1021	ATTCTTCCCAATCTTTATCTTGGCTGCCAGCGAGATGTCTCAACAAGGAGCTGATACAG	1080
162	I L P N L Y L G C Q R D V L N K E L I Q	181
1081	CAGAATGGGATTGGTTATGTGTTAAATGCCAGCTATACCTGTCCAAAGCCTGACTTTATC	1140
182	Q N G I G Y V L N A S Y T C P K P D F I	201
1141	CCCGAGTCTCATTTCCTGCGTGTGCCTGTGAATGACAGCTTTTGTGAGAAAATTTTGCCG	1200
202	P E S H F L R V P V N D S F C E K I L P	221
1201	TGGTTGGACAAATCAGTAGATTTTCATTGAGAAAGCAAAGCCTCCAATGGATGTGTTCTA	1260
222	W L D K S V D F I E K A K A S N G C V L	241
1261	GTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACCATCGCTATCGCCTACATCATGAAG	1320
242	V H C L A G I S R S A T I A I A Y I M K	261
1321	AGGATGGACATGTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAGACCTACTATA	1380
262	R M D M S L D E A Y R F V K E K R P T I	281
1381	TCTCCAAACTTCAATTTTCTGGGCCAACTCCTGGACTATGAGAAGAAGATTAAGAACCAG	1440
282	S P N F N F L G Q L L D Y E K K I K N Q	301
1441	ACTGGAGCATCAGGGCCAAAGAGCAAACCTCAAGCTGCTGCACCTGGAGAAGCCAAATGAA	1500
302	T G A S G P K S K L K L L H L E K P N E	321
1501	CCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGCGAGACGCCCTCAGTCCACCCTGT	1560
322	P V P A V S E G G Q K S E T P L S P P C	341
1561	GCCGACTCTGCTACCTCAGAGGCAGCAGGACAAAGGCCCGTGCATCCCGCCAGCGTGCCC	1620
342	A D S A T S E A A G Q R P V H P A S V P	361
1621	AGCGTGCCCAGCGTGCAGCCGTCGCTGTTAGAGGACAGCCCGCTGGTACAGGCGCTCAGT	1680
362	S V P S V Q P S L L E D S P L V Q A L S	381
1681	GGGCTGCACCTGTCCGCAGACAGGCTGGAAGACAGCAATAAGCTCAAGCGTTCCTTCTCT	1740
382	G L H L S A D R L E D S N K L K R S F S	401
1741	CTGGATATCAAATCAGTTTCATATTCAGCCAGCATGGCAGCATCCTTACATGGCTTCTCC	1800
402	L D I K S V S Y S A S M A A S L H G F S	421
1801	TCATCAGAAGATGCTTTGGAATACTACAAACCTTCCACTACTCTGGATGGGACCAACAAG	1860
422	S S E D A L E Y Y K P S T T L D G T N K	441

Figure 19C

1861	CTATGCCAGTTCTCCCCTGTTTCAGGAACTATCGGAGCAGACTCCCGAAACCAGTCCTGAT	1920
442	L C Q F S P V Q E L S E Q T P E T S P D	461
1921	AAGGAGGAAGCCAGCATCCCCAAGAAGCTGCAGACCGCCAGGCCTTCAGACAGCCAGAGC	1980
462	K E E A S I P K K L Q T A R P S D S Q S	481
1981	AAGCGATTGCATTTCGGTCAGAACCAGCAGCAGTGGCACCAGCCAGAGGTCCCTTTTATCT	2040
482	K R L H S V R T S S S G T A Q R S L L S	501
2041	CCACTGCATCGAAGTGGGAGCGTGGAGGACAATTACCACACCAGCTTCCTTTTCGGCCTT	2100
502	P L H R S G S V E D N Y H T S F L F G L	521
2101	TCCACCAGCCAGCAGCACCTCACGAAGTCTGCTGGCCTGGGCCTTAAGGGCTGGCACTCG	2160
522	S T S Q Q H L T K S A G L G L K G W H S	541
2161	GATATCTTGGCCCCCAGACCTCTACCCCTTCCCTGACCAGCAGCTGGTATTTTGCCACA	2220
542	D I L A P Q T S T P S L T S S W Y F A T	561
2221	GAGTCCTCACACTTCTACTCTGCCTCAGCCATCTACGGAGGCAGTGCCAGTTACTCTGCC	2280
562	E S S H F Y S A S A I Y G G S A S Y S A	581
2281	TACAGCTGCAGCCAGCTGCCCCACTTGCGGAGACCAAGTCTATTCTGTGCGCAGGCGGCAG	2340
582	Y S C S Q L P T C G D Q V Y S V R R R Q	601
2341	AAGCCAAGTGACAGAGCTGACTCGCGGCGGAGCTGGCATGAAGAGAGCCCCTTTGAAAAG	2400
602	K P S D R A D S R R S W H E E S P F E K	621
2401	CAGTTTAAACGCAGAAGCTGCCAAATGGAATTTGGAGAGAGCATCATGTGAGAGAACAGG	2460
622	Q F K R R S C Q M E F G E S I M S E N R	641
2461	TCACGGGAAGAGCTGGGGAAAGTGGGCAGTCAGTCTAGCTTTTCGGGCAGCATGGAAATC	2520
642	S R E E L G K V G S Q S S F S G S M E I	661
2521	ATTGAGGTCTCCTGAGAAGAAAGACACTTGTGACTTCTATAGACAATTTTTTTTTTCTTG	2580
662	I E V S	665
2581	TTCACAAAAAAATCCCTGTAAATCTGAAATATATATATGTACATACATATATATTTTG	2640
2641	GAAAATGGAGCTATGGTGTAAGCAACAGGTGGATCAACCCAGTTGTTACTCTCTTAAC	2700
2701	ATCTGCATTGAGAGATCAGCTAATACTTCTCTCAACAAAAATGGAAGGGCAGATGCTAG	2760
2761	AATCCCCCTAGACGGAGGAAAACCATTTTATTTCAGTGAATTACACATCCTCTTGTTCTT	2820

Figure 19D

2821 AAAAAAGCAAAGTGTCTTTGGTGTGGAGGACAAAATCCCCTACCATTTTACGTTGTGCT 2880
 2881 ACTAAGAGATCTCAAATATTAGTCTTTGTCCGGACCCTTCCATAGTACACCTTAGCGCTG 2940
 2941 AGACTGAGCCAGCTTGGGGGTGAGGTAGGTAGACCCTGTTAGGGACAGAGCCTAGTGGTA 3000
 3001 AATCCAAGAGAAATGATCCTATCCAAAGCTGATTACAAACCCACGCTCACCTGACAGCC 3060
 3061 GAGGGACACGAGCATCACTCTGCTGGACGGACCATTAGGGGCCTTGCCAAGGTCTACCTT 3120
 3121 AGAGCAAACCCAGTACCTCAGACAGGAAAGTCGGGGCTTTGACCACTACCATATCTGGTA 3180
 3181 GCCCATTTTCTAGGCATTGTGAATAGGTAGGTAGCTAGTCACACTTTTCAGACCAATTCA 3240
 3241 AACTGTCTATGCACAAAATTCCCGTGGGCCTAGATGGAGATAATTTTTTTTCTTCTCAG 3300
 3301 CTTTATGAAGAGAAGGGAAACTGTCTAGGATTGAGCTGAACCACCAGGAACCTGGCAACA 3360
 3361 TCACGATTTAAGCTAAGGTTGGGAGGCTAACGAGTCTACCTCCCTCTTTGTAAATCAAAG 3420
 3421 AATTGTTTTAAATGGGATTGTCAATCCTTTAAATAAAGATGAACTTGGTTTCAAGCCAAA 3480
 3481 TGTGAATTTATTTGGGTTGGTAGCAGAGCAGCAGCACCTTCAAATTCTCAGCCAAAGCAG 3540
 3541 ATGTTTTTGGCCCTTTCTGCTTCACTGCATGGATACAGTTGGTAAAATGTAATAATATGGC 3600
 3601 AGAATTTTATAGGAACTTCCTAGGGAGGTAAATTATGGGAAGATTAAGAAAGGTACAAA 3660
 3661 TTGCTGAGGAGAAGCAGGAAACCTGTTTCCTTAGTGGCTTTTATCCCCTCGGCATGCGAT 3720
 3721 GGGGCTGATGTTTCTATGATTGCCTCAGACTTTCACATTTACTAGTAGGGCTGAGAGAGG 3780
 3781 CTTTAGTGAGGAAGGAATATTCAGAATAAAACGGTTGAGAAAGCTGAGAAGACCATTGAG 3840
 3841 TTTTGATCAGTTGTGAATAGAGTGCAAAGCCATGGCCAAGCTGTTTTTGGAAACGCTGGC 3900
 3901 CGGCGTGTCTTCAGTGGAAGAAAGCAAATCAAATGGAGCGAGAGCAAAGGGGCGTCTCA 3960
 3961 GTCCTCAACCTACAATCACTGTATGGAATCGGTCCTGGCAGCTGAACATAGGAGGTCACT 4020

Figure 19E

4021 GGAACAAGTGATAGTGCAGATTGGCTTTCAAACATCCTCCTGGCTTGAGTTTTATCAGCT 4080
 4081 ACAATGTGGGTCCCTCTTTTGAAGCCTTAATTCACAACAGCAGCTTTTTGGGGTGGGGCT 4140
 4141 GGGCGGGTGTGTCATTGTTCTTTCCCTTCCTGTAAGTGTCGCTAGTTGCTGCCTCGTAT 4200
 4201 CTCAGGTTTTTCTCTGTTTTTGAGAAATGGACAGTTTTTTGACCAGGATGTGACTTCATG 4260
 4261 TTTCTATGGTGACTTCTAAAACCAGCACAGAATGATATGACTCAACACAGACCGACTTG 4320
 4321 GTTATGGGGATGATGAGCCGCACAGACCTCACTAGTTGTGCACAAATAATGTGCTATGAT 4380
 4381 GGGGTGTAAAGTGAAGGCAGAAGAGGGTCAGCCGCATTGTTATGATACTGGGAAAGTGCT 4440
 4441 GGTCAACGATTTGAGTTAGTTTTTAGATATACATTGAAATCTTTAATCAGACATTCTCAA 4500
 4501 GTTTCACACAGTAGTTTTTGATGTTATGTACACACACACCAAATGTGTAACAGTTCACCA 4560
 4561 CTTCCAGAGTGTGGTCATGCCCAAAACATGTTTAAGAAAGGAAAGCAGTAGCTCCTTGCT 4620
 4621 AACGATGTTTCAGGAGGTTTGGGGCACTTGGTTTTAATGAGCTTCTGTCATTTAGGGCTT 4680
 4681 CTCTTGCCCATGGTCCCCCTTCTTCTGGAACGTGTGATGTAGTCACATCCTACAGCCTTTA 4740
 4741 GTGCTGGTTCACTAGTGTGAGATAATCAGTTCTTGAATCGAGACTGCCGTGGCGAAGGG 4800
 4801 GTGGCCTCGGAGGCAGGCTCTGGAGCTGCTTGGATGTCTTTAGGTGGGGTGGTGGCTGGC 4860
 4861 TCTCTTCAGCATGTAATTGGGGAACCCTCGCGTCTACTAGGGGTGATACAGATGGTGAT 4920
 4921 TTTAAAGAGCAAACTAGACTTCTATGTGAGAAGTGCTGGAAAATGATTTAGGACATGTG 4980
 4981 TAAAGTTAGATGGAAAGACTGTAAATGTTTAATATGAATATAGTGTTCTTTTGAAGTAAG 5040
 5041 GCCAGCTGTTGAACGGTTAAACTGTGCATTTCTCATTTTGATGTGTCATGTATGTTAATG 5100
 5101 TATGAAATGATTAAATAAAATCAAACTGCTACCTGTTTATACATAAATACGAGAAAAGA 5160

Figure 19F

5161 CCTATCTTTGCAGCCATAAACTCGGTGGGAACACCACCACTCAAGTTGCCAAAGGAGGCA 5220
5221 GTGGTGAAACCTGTCCTGTTCTCACTTAAATGAGGATTTAGCTCAAATAAAGTGGTGGT 5280
5281 GTCATCAGGTTTATTCCGTGTTCTGTCATTACATGGAACACCGGATGATTAGCTAACAG 5340
5341 TTTAGTGCCAGCCTTCATTCTTTACTGTGTACGTTAAATGCACACTACAGTGAAAAAGCC 5400
5401 TAAGACACTTGGTAAATATTTTCTAGCTGACTGATTCCAGAACACACAAG 5450

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Figures 20A

1 CCACGCGTCCGGCTCTTGCTCCCACTGCCATGCAGGTGCAGGATGCAACCAGGCGGCCC 60
61 TCAGCCGTGCGCTTCCTCAGCTCCTTTCTCCAGGGCCGCCGGCACTCCACCTCAGACCCA 120
121 GTACTGCGGCTGCAGCAGGCCCGCGGGGCTCTGGCTTGGGCTCCGGCTCTGCCACGAAG 180
181 CTGCTGTCTCTCGTCTCTCTCCAGGTGATGGTGGCTGTTTCTCAGTCAGCCATGCAGAG 240
241 GGAAACCCAACCTTTCCCCGAAAGAAAAGAAATTTAGAACGTCCAACACCAAAGTACACA 300
301 AAAGTAGGGGAGCGTTTACGGCATGTCATTCTGGACACATGGCATGTTCCATGGCGTGT 360
361 GGCGGTAGAGCTTGCAAGTATGAGAACCCAGCCCGCTGGAGTGAGCAGGAGCAAGCCATT 420
421 AAGGGGGTTTACTCATCTCTGGGTCACTGATAATATACTGGCCATGGCCCGCCCATCTCT 480
481 GAGCTCCTGGAGAAGTACCACATCATTGATCAGTTCCTCAGCCATGGCATAAAAAACAATA 540
541 ATCAACCTCCAGCGCCCTGGTGAGCATGCTAGCTGTGGGAACCCTCTGGAACAAGAAAGT 600
601 GGCTTCACATACCTTCTGAGGCTTTTCATGGAGGCTGGCATTACTTCTACAATTTCCGA 660
1 M E A G I Y F Y N F G 11
661 TGGAAGGATTATGGTGTAGCGTCTCTTACTACTATCCTAGATATGGTGAAGGTGATGACA 720
12 W K D Y G V A S L T T I L D M V K V M T 31
721 TTTGCCTTACAGGAAGGAAAAGTAGCTATCCATTGTCATGCAGGGCTTGGTTCGAACAGGT 780
32 F A L Q E G K V A I H C E A G L G R H G 51
781 GTTTTAATAGCCTGTTACTTAGTTTTTGCAACGAGAATGACTGCTGACCAAGCAATTATA 840
52 V L I A C Y L V F A T R M T A D Q A I I 71
841 TTTGTGCGGGCAAAGCGACCCAATTCCATACAAACCAGAGGACAGCTCCTCTGTGTAAGG 900
72 F V R A K R P N S I Q T R G Q L L C V R 91
901 GAATTTACTCAGTTTCTAACTCCTCTCCGCAATATATTCTCTTGCTGTGATCCCAAAGCA 960
92 E F T Q F L T P L R N I F S C C D P K A 111
961 CATGCTGTACCTTACCTCAATATCTAATTCGCCAGCGTCATCTGCTTCATGGTTATGAG 1020
112 H A V T L P Q Y L I R Q R H L L H G Y E 131
1021 GCACGACTTCTGAAACACGTGCCAAAAATATCCACCTAGTTTGCAAATTGCTGCTGGAC 1080
132 A R L L K H V P K I I H L V C K L L L D 151
1081 TTAGCGGAGAACAGGCCAGTGATGATGAAGGATGTGTCCGAAGGACCTGGTCTCTCTGCT 1140
152 L A E N R P V M M K D V S E G P G L S A 171

Figures 20B

1141 GAAATAGAAAAGACAATGTCTGAGATGGTCACCATGCAGCTGGATAAAGAGTTACTGAGG 1200
 172 E I E K T M S E M V T M Q L D K E L L R 191

1201 CATGACAGTGATGTGTCCAACCCGCCTAACCCCACTGCAGTGGCAGCAGATTTTGACAAT 1260
 192 H D S D V S N P P N P T A V A A D F D N 211

1261 CGAGGCATGATTTTCTCCAATGAGCAACAGTTTGACCCTCTTTGGAAAAGGCGGAATGTT 1320
 212 R G M I F S N E Q Q F D P L W K R R N V 231

1321 GAGTGCCTTCAACCCCTGACTCATCTGAAAAGGCGGCTCAGCTACAGTGAAGTCAAGTTTA 1380
 232 E C L Q P L T H L K R R L S Y S D S D L 251

1381 AAGAGGGCCGAGAACCTCCTGGAGCAAGGGGAGACTCCACAGACAGTGCCTGCCCAGATC 1440
 252 K R A E N L L E Q G E T P Q T V P A Q I 271

1441 TTGGTTGGCCACAAGCCCAGGCAGCAGAAGCTCATAAGCCATTGTTACATCCCACAGTCT 1500
 272 L V G H K P R Q Q K L I S H C Y I P Q S 291

1501 CCAGAACCAGACTTACACAAGGAAGCCTTGGTTCGCAGCACACTTTCTTTCTGGAGTCAG 1560
 292 P E P D L H K E A L V R S T L S F W S Q 311

1561 TCAAAGTTTGGAGGCCTGGAAGGACTCAAAGATAATGGGTACCAATTTTCCATGGAAGG 1620
 312 S K F G G L E G L K D N G S P I F H G R 331

1621 ATCATTCCAAAGGAAGCACAGCAGAGTGGAGCTTTCTCTGCAGATGTTTCAGGCTCACAC 1680
 332 I I P K E A Q Q S G A F S A D V S G S H 351

1681 AGCCCTGGGGAGCCAGTTTCAACCCAGCTTTGCAAATGTCCATAAGGATCCAAACCCTGCT 1740
 352 S P G E P V S P S F A N V H K D P N P A 371

1741 CACCAGCAAGTGTCTCACTGTCAAGTGTAAACTCATGGTGTGGAGCCCTGGCTCTGTC 1800
 372 H Q Q V S H C Q C K T H G V G S P G S V 391

1801 AGGCAGAACAGCAGGACACCCGAAGCCCTCTGGACTGTGGCTCCAGTCCCAAAGCACAG 1860
 392 R Q N S R T P R S P L D C G S S P K A Q 411

1861 TTCTTGGTTGAACATGAAACCCAGGACAGTAAAGATCTGTCTGAAGCAGCTTCACACTCT 1920
 412 F L V E H E T Q D S K D L S E A A S H S 431

1921 GCATTACAGTCTGAATTGAGTGTGAGGCAAGAAGAATACTGGCGGCCAAAGCCCTAGCA 1980
 432 A L Q S E L S A E A R R I L A A K A L A 451

1981 AATTTAAATGAATCTGTAGAAAAGGAGGAATAAAAGGAAGGTAGAAATGTGGCAGAAA 2040
 452 N L N E S V E K E E L K R K V E M W Q K 471

2041 GAGCTTAATTCCTGAGATGGAGCTTGGGAAAGAATATGTGGCGAGAGGGACCCTTTTCATC 2100
 472 E L N S R D G A W E R I C G E R D P F I 491

Figures 20C

2101 CTATGCAGCTTGATGTGGTCTTGGGTGGAGCAACTGAAGGAGCCTGTAATCACCAAAGAG 2160
492 L C S L M W S W V E Q L K E P V I T K E 511

2161 GATGTGGACATGTTGGTTGACAGGCGAGCAGATGCCGCGAGAAGCACTTTTTTATTAGAG 2220
512 D V D M L V D R R A D A A E A L F L L E 531

2221 AAGGGACAGCACCAGACTATTCTCTGCGTGTGCACTGCATAGTAACCTGCAGACAATT 2280
532 K G Q H Q T I L C V L H C I V N L Q T I 551

2281 CCCGTGGATGTGGAGGAAGCTTTCCTTGCCCATGCCATTAAGGCATTCACTAAGGTAAAT 2340
552 P V D V E E A F L A H A I K A F T K V N 571

2341 TTTGATTCTGAAAAATGGACCAACAGTTTACAACACCCTGAAGAAAATATTTAAGCACACG 2400
572 F D S E N G P T V Y N T L K K I F K H T 591

2401 CTGGAAGAAAAAAGAAAAATGACAAAAGATGGCCCTAAGCCTGGCCTCTAGCTTTCACCTC 2460
592 L E E K R K M T K D G P K P G L * 607

2461 ATGGTGAATATTTTACAGACCTAAAGATCCAGATAGTATCTCTGTTTCATATGTGAATAAGTT 2520

2521 GAAGATTGTGGGGCTACTTTTCTCATAGCACTTTATTTTGAATGTTGTTAGTTTGTGCT 2580

2581 GAGAATGGTCGTCCGTATTTGAACCAATTATTTATTTTAAATATATTTAAGCTACATTT 2640

2641 TTGTTTTGAAAAATTGCCATAAATTGGTGCCACTTCTTTTATTTATTTGACTGAGTTA 2700

2701 ATATTATTGTATTAACATTTTAAGTATATGGTGTTTACATTCTTATTTCTTTTGACATTT 2760

2761 TGGAAATAATCATAACTTGTCTTTCCAAAATAACCATTTTCTTGATGGAACCTCTCCTAG 2820

2821 AGTTTTTACCAAATAGCTAACTTTAGTAGTAAACCTCATTGTGTATCCATTCCCCCACA 2880

2881 GATGAACTAAGAAAGTCACCAAGTGTCTTAAGCTGTTTTATATTTGTTACGAAGAAGGCT 2940

2941 ATTGCTACAATATTTTAAAGGTTCTTTTTTAACTTTGAAATTTTTTGTTTTTCCTTTT 3000

3001 CTTTTTATAAATGTAACAGAGGTTTCAAAGCATATTATTTTTCAGAGAGATTTAGTTTT 3060

3061 ACTTTAATGGAGTGACTGTGAAGTGTTGGGATTTTTTGCTTGTAGAAAGTAGACTTGCT 3120

3121 CTTTGTGAGATTTCCAAACAACCTTGCCAGCCTTGGCTGTCAAAGGAGGCAGGAGCAGT 3180

3181 TCTCAACACACCAAGCCTTATCCCACTCCCTTGGGTGCTGCTGAGCCAAATAGCATCT 3240

3241 TTACAGAGGAAGTGGGATCAGAGGCAGGAAGTGTGGAAAGTTGCTAAGAAGCAGGGCTTG 3300

Figures 20D

3301 CCTCTGTCCTCCCGGGGACTCCACAGGGATATTCGTGCAGGGCAGGGGCTCTGTGCCAGC 3360
 3361 CCTGCTCTCTCAGATGCCACAGCCACTCTGCAGAGGTGACTCTTGGAGCTGGAGGAAGTC 3420
 3421 AAAACTGGGCCACTGTTTGTACTGATGGTGTATTAGCATGAGCAGCGTGGCCCTGGCCCC 3480
 3481 AACTCCCAAATCTGCCACTCCATAGACCCACTTGCCTCAAGGCTTTATATTTGGCTGCT 3540
 3541 TTCTTACAATGAGAATTAAGATTTTTTAACTGAAGTTGACCATACAGGTTGCATTAGCCC 3600
 3601 TAACTGGCTTCATGTAAGAAGGGTGACTGCCTAACTAGTTCCTTGTAAGCTGAACCATC 3660
 3661 AATTATCAGTTGAAGCCATACTTTTATTTAAATTAATATACGTAGATACCAGAGGCCAAG 3720
 3721 CCACAGAGAGGATAATAGTTCTTCCCAATAAAGGTGATATTAATCAGACTAATTTGGAAC 3780
 3781 TAAAGAAGTTACTGCTTAAAGACGGAATTTTCAAGGGAAGCAAGACTCATTTAGAACAAT 3840
 3841 GAAATTTCTCCAGTCTTACATTTCTGAATTGACTTCTAGCACATCAAAAATATTTAGTC 3900
 3901 ATTATCAGTCTCATTAACTGAAATGCCAAATGCTAAATGCAGTGTCTTTTCACTGTTT 3960
 3961 TAATTTTCTTGGGAAATTGAGTCCAGTGGATGTTAATGGAGTGGGTGCCCATCCCTGAA 4020
 4021 ATGTCTTATTTTCAAGTGCCTGGCCTGGGAAAGAAGGGAAGAAACAATTGCATTATATC 4080
 4081 CAAAGATACACTATAAAAAATAGAGTTTTTACCAAAAAAAGATGTTTGTCTCATCTCAGT 4140
 4141 AGGCCTCATTTGGGCAAGTGACCCACAGGTCTTTTGGCGAGTTTGCTATTTGCCTGTTGA 4200
 4201 AATACTTGTTTCACTTAGAGAACAGTTATGATGTGACCATAGCATGGCACAATAAAAA 4260
 4261 TCTAAGCCTGAAACCTGAAAAAGAGATATGACAAGGGAATTAATCAGGCTATACATAA 4320
 4321 GTATTGTATTTATTTGAATAAAAAATAAAAGAGCAACCCATAAAAAAAAAAAAAAAAAAA 4380
 4381 AAAAAAAAAAAG 4393

Figures 21

1 CCACGCGTCCGGCGAGGGGACGCGTGGGCGGAGCGGGGCTGGCCAGCCTCGGCCCCCATG 60
61 ACCCGCTGTCTGTGCCCTTTCCAGCGATGGGCGTGCAGCCCCCACTTCTCCTGGGT 120
1 M G V Q P P N F S W V 11
121 GCTTCGGGCGGCTGGGCGGACTGGGCGTGCCGCGGCTCCCCGCCCCTACAGTTCCT 180
11 L P G R L A G L A L P R L P A H Y Q F L 31
181 GTTGGACCTGGGCGTGGGCGACCTGGTGTCCCTGACGGAGCGGGGCCCTCACAGCGA 240
31 L D L G V R H L V S L T E R G P P H S D 51
241 CAGCTGCCCCGGCCTCACCTGCACCGCCTGCGCATCCCCGACTTCTGCCCCGGGCCCC 300
51 S C P G L T L H R L R I P D F C P P A P 71
301 CGACCAGATCGACCGCTTCGTGCAGATCGTGGACGAGGCCAACGCACGGGGAGAGGCTGT 360
71 D Q I D R F V Q I V D E A N A R G E A V 91
361 GGGAGTGCCTGTGCTCTGGGCTTTGGCCGCACTGGCACCATGCTGGCCTGTTACCTGGT 420
91 G V H C A L G F G R T G T M L A C Y L V 111
421 GAAGGAGCGGGGCTTGCTGCAGGAGATGCCATTGCTGAAATCCGACGACTACGACCCGG 480
111 K E R G L A A G D A I A E I R R L R P G 131
481 CTCCATCGAGACCTATGAGCAGGAGAAAGCAGTCTTCCAGTTCTACCAGCGAACGAAATA 540
131 S I E T Y E Q E K A V F Q F Y Q R T K * 150
541 AGGGGCCTTAGTACCCTTCTACCAGGCCCTCACTCCCCTTCCCCATGTTGTCGATGGGGC 600
601 CAGAGATGAAGGGAAGTGGACTAAAGTATTAAACCCTCTAGCTCCCATTGGCTGAAGACA 660
661 CTGAAGTAGCCACCCCTGCAGGCAGGTCTGATTGAAGGGGAGGCTTGTA CTGCTTTGT 720
721 TGAATAAATGAGTTTACGAACCAGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 780
781 AA 840
841 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGC 878

Figure 22

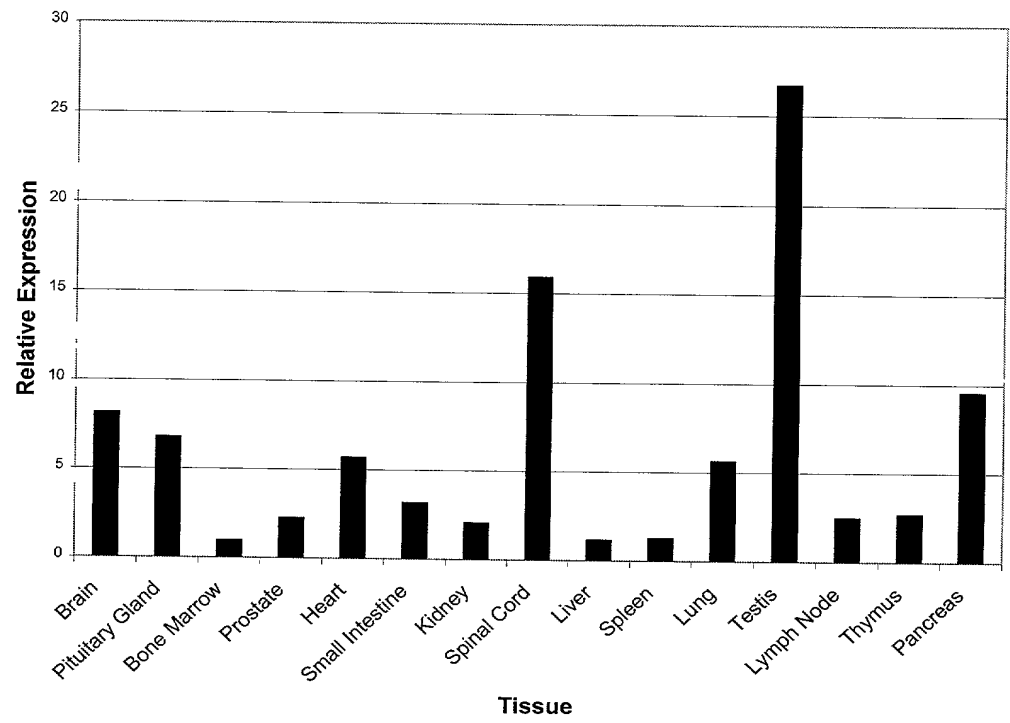


Figure 23

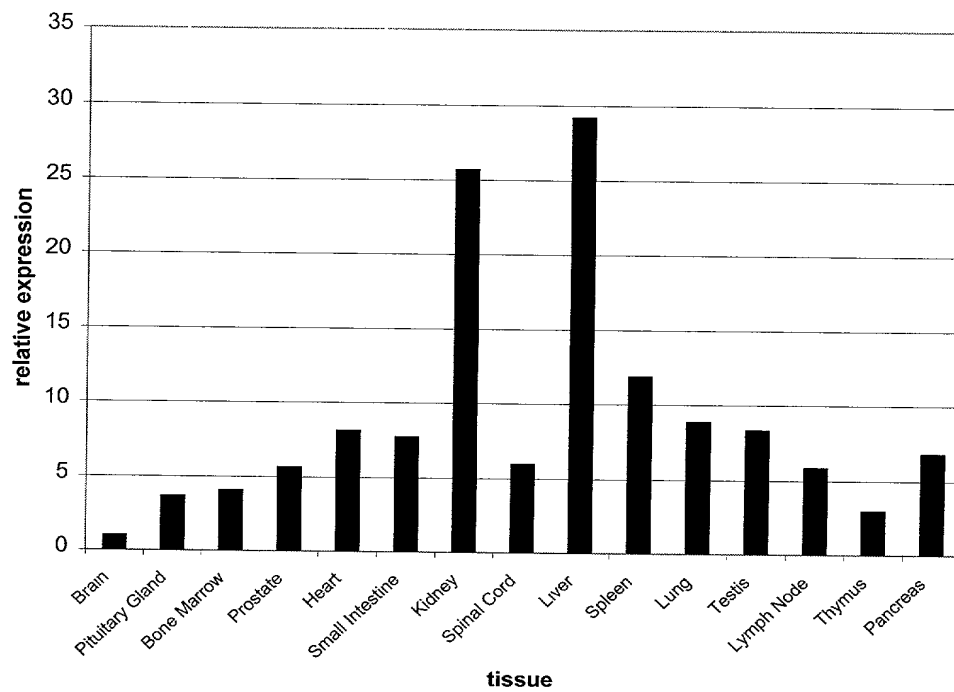


Figure 24.

BMY_HPP1

<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human protein tyrosine phosphatase	gi P32587	27%	39.6%
mouse protein tyrosine phosphatase	gi NP_035346	27.9%	40.5%
Schizosacchromyces Pombe protein tyrosine phosphatase PYP3 protein	gi NP_002839	27.5%	36.7%

BMY_HPP2

<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human S. cerevisiae CDC14 homolog A	gi NP_003663	33.1%	44.1%
human S. cerevisiae CDC14 homolog B	gi NP_003662	33.1%	45.8%
yeast soluble tyrosine-specific protein phosphatase Cdc14p protein	gi NP_002839	33.1%	45.8%

Figure 25.

RET31			
<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human protein-tyrosine phosphatase DUS8 protein	gi U27193	50.3%	56.8%
the human dual specificity MAP kinase DUSP6 protein	gi AB013382	36.5%	48.3%
human map kinase phosphatase MKP-5 protein	gi AB026436	34.3%	47.2%
mouse RET31 protein	N/A	90%	92%

Figure 26

Relative Abundance of BMJ_HPP1 in Normal Tissues

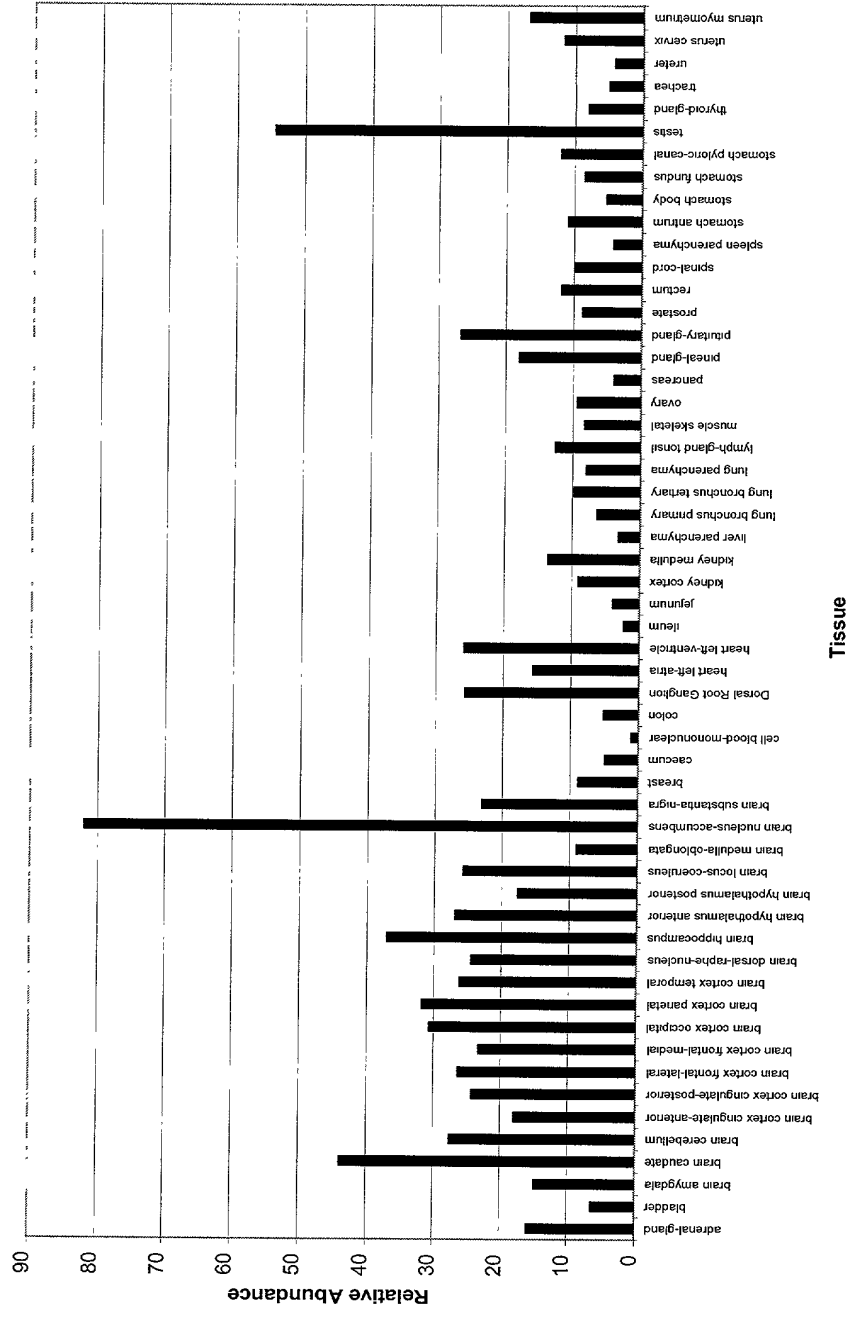
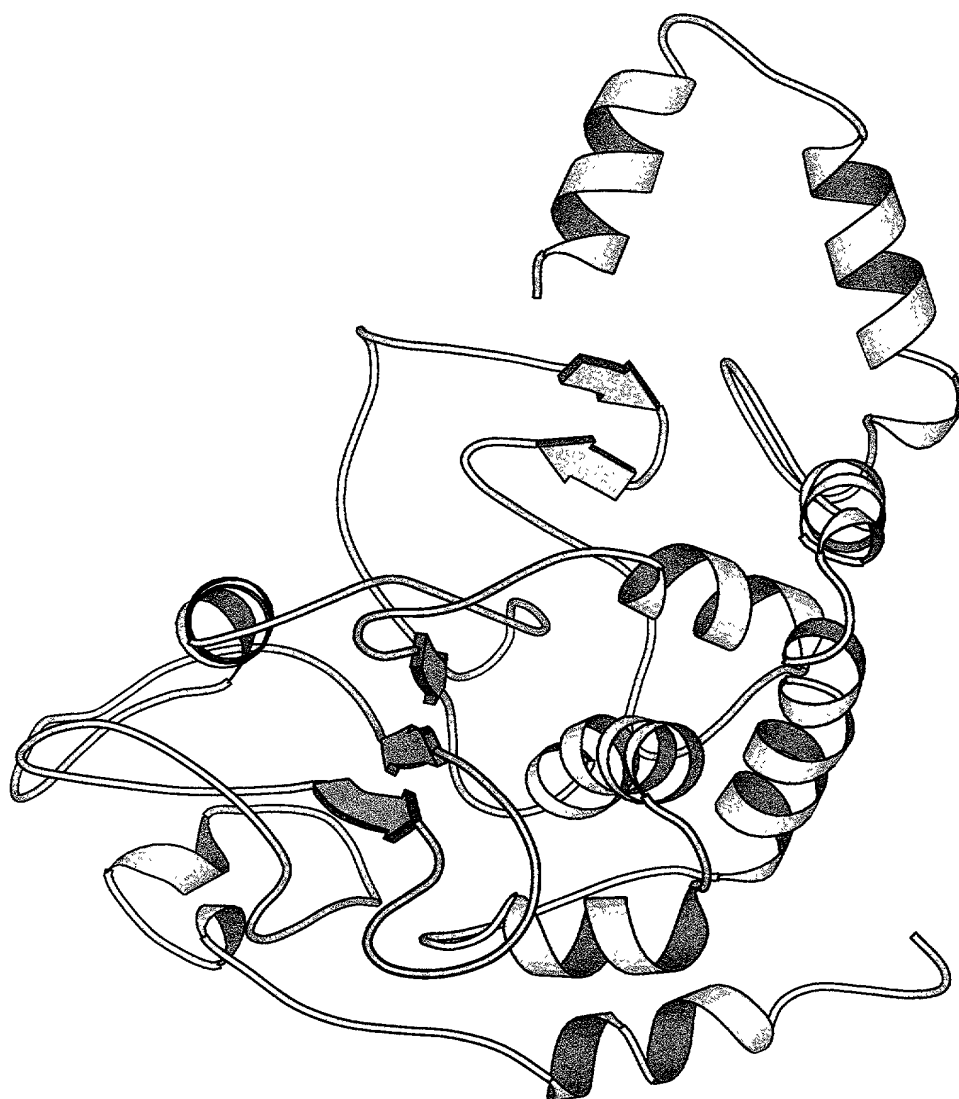


Figure 27

HPP1	MAAGVLPQNE	QPYSTLVNNS	EC.VANMKGN	LERPTPKYTK	39
pdblaax	MEMEKEFEQI	DKSGSWAAIY	QDIRHEASDF	PCRVAKLPKN	KNRNRYRDVS	50
HPP1	VGERLRHVIP	GHMCSMACG	GRACKYENPA	RWSEQEQAIAK	GVYSSWVTDN	89
pdblaax	PFDH..SRIK	LHQEDNDYIN	ASLIKME...EAQRS	YILTQGPLPN	90
HPP1	ILAMARPSSE	LLEKYHIIDQ	FLSHGIKTII	NLQRPGE..H	ASCGNPLEQE	137
pdblaaxTCGHFWEM	VWEQKSRGVV	MLNRVMEKGS	LKCAQYWPOK	128
HPP1	S.....GFTYL	PEAFMEAG..IYFYNFG	158
pdblaax	EEKEMIFEDT	NLKLTLISED	IKSYTTRVQL	ELENLTQTET	REILHFHYTT	178
	**			** *	*	
HPP1	WKDYGVA.SL	TTILDMVKVM	...TFALQE	GKVAIHCHAG	LGRTGVLIAC	203
pdblaax	WPDFGVPESP	ASFLNFLFKV	RESGSLSPFH	GPVVVHSSAG	IGRSGTFCLA	228
HPP1	YLVFATR...MTADQ	AIIFVRAKRP	NSI....QTR	GQLLCVREFT	241
pdblaax	DTCLLLMDKR	KDPSSVDIKK	VLLEMRKFRM	GLIQTADQLR	FSYLAVIEGA	278
HPP1	QFLTPLRNIF	SCCDPKAHAV	TLPOYLIRQR	HLLHGYEARL	LKHVPKIIHL	291
pdblaax	KFIM.....	GDSSVQDQWK	ELSHEDLEPP	PGHIPPPPRP	312
HPP1	VCKLLLDLAE	NRPVMMKDVS	EGPGLSAEIE	KTMSEMVTMQ	LDKELLRHDS	301
pdblaax	PKRILEPHN.	321

Figure 28



HPP1 Homology Model

Figure 29

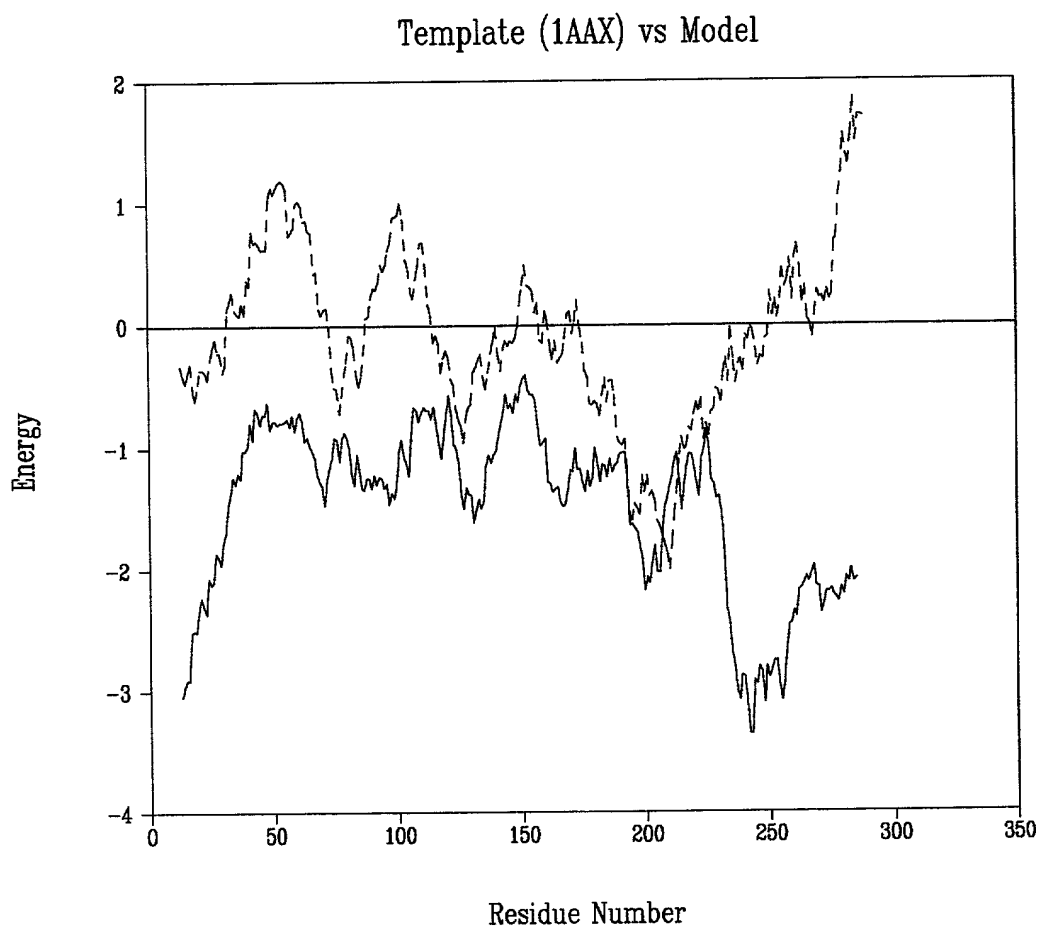


Figure 30

Figure 30

Relative Abundance of BMJ_HPP2 in Normal Tissues

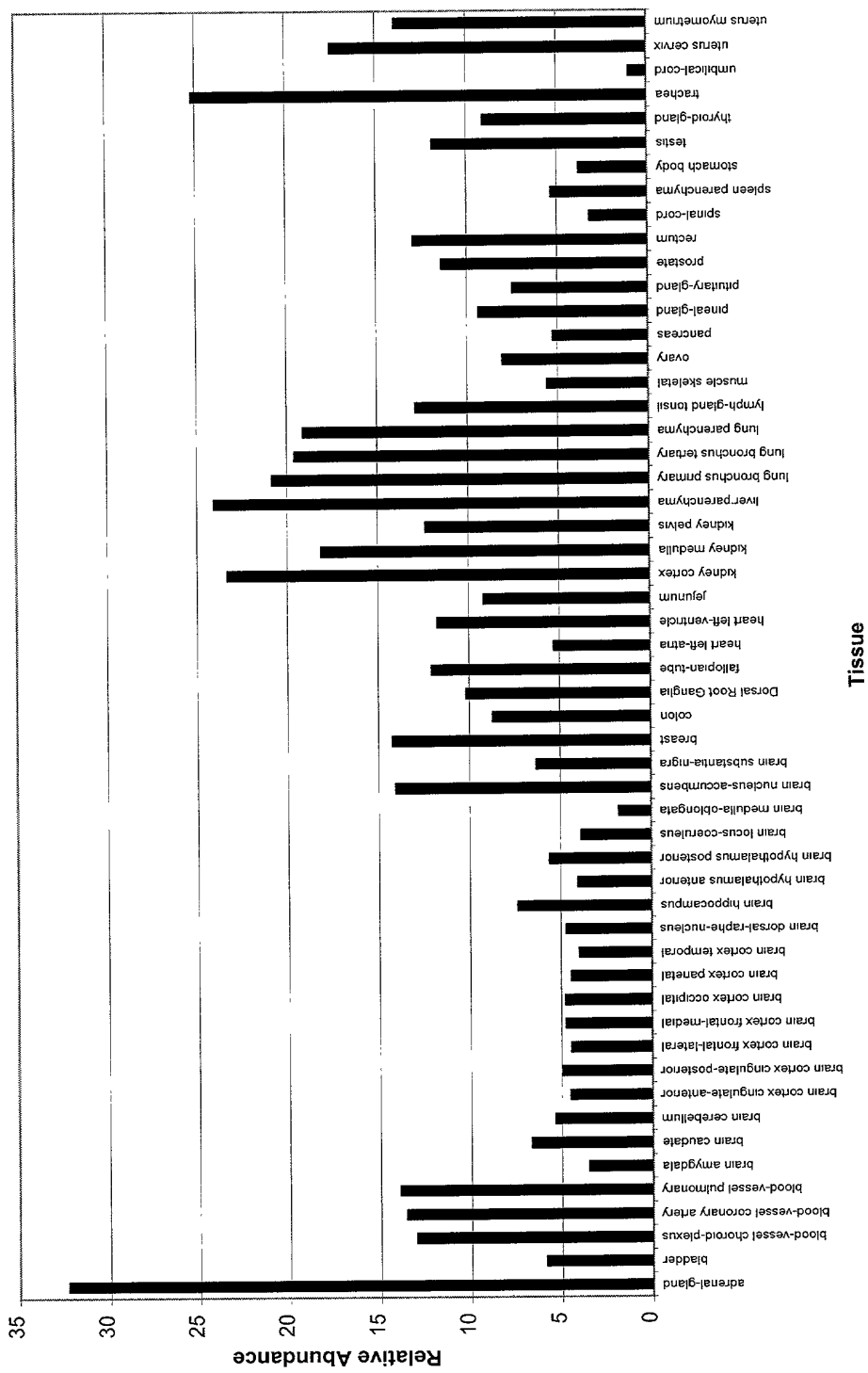


Figure 31

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      20      30      40      50      60      70
pdblvrA GCYSLPSQPCNEVTPRIYVGNASVAQDIPKLQKLGITHVLNAAEGRSEFMHVNTNANFYKD
      :  ::  ....  ::  ::  :  ..
BMY_HPP2 MGVPFNFVSWVLPGRLAGLALPRLPAHYQFLDLGVRHLVSLTE-RGPPHSDSCP-----
      10      20      30      40      50

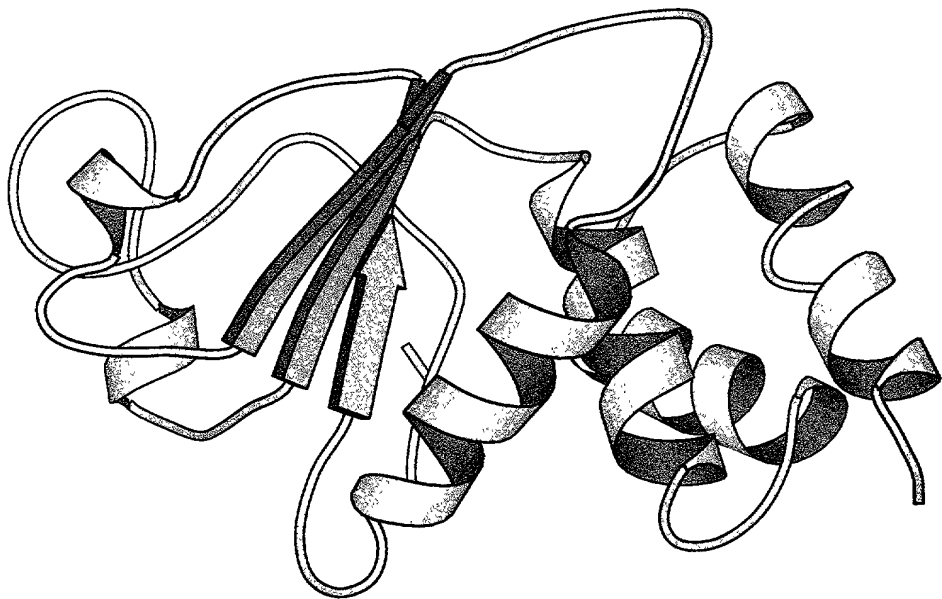
      80      90      100      110      120      130
pdblvrA SGITYLGIKANDTQEFNLSA--YFERAADFIDQALAQKNGRVLVHCREGYRSPTLVIAY
      ::  ..  :  :  :  ...  ::  ::  :  ::  :  ::  :  ::  :  ::  :  ::  :
BMY_HPP2 -GLTLHRLRIPD---FCPPAPDQIDRFVQIVDEANARGEA-VGVHICALGFGRGTGTMLACY
      60      70      80      90      100

      140      150      160      170      180
pdblvrA LMMRQKMDVKSALSIVRQNREIGPNDGFLAQLCQLNDRLAKEGKLP
      :  .  .  .  .  .  .  .  :
BMY_HPP2 LVKERGLAAGDAIAEIRRLRPGSIETYEQEKAVFQFYQRTK
      110      120      130      140      150

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Figure 32



HPP2 Homology Model

Figure 33

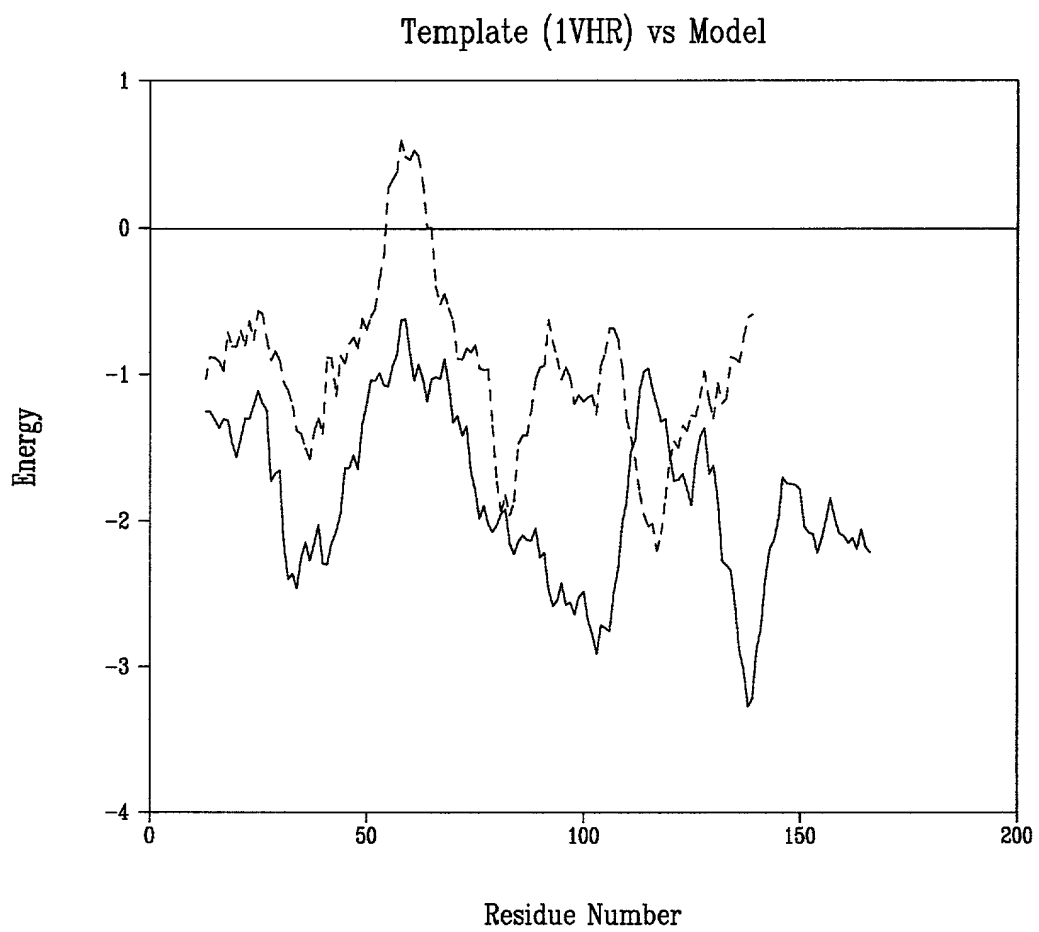


Figure 34

Relative Abundance of BMJ_HPP4 in Normal Tissues

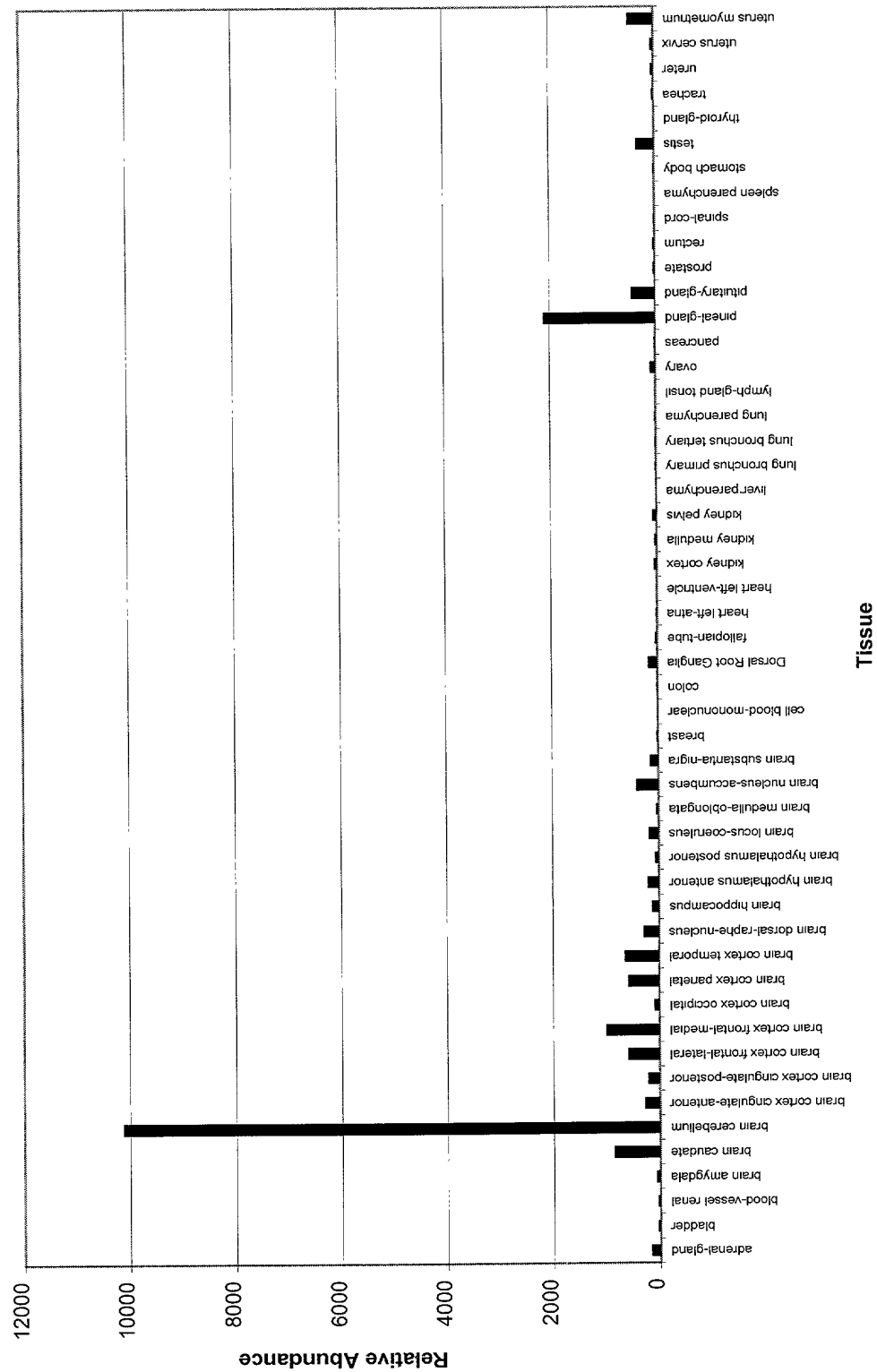


Figure 35

Relative Abundance of BMJ_HPP5 in Normal Tissues

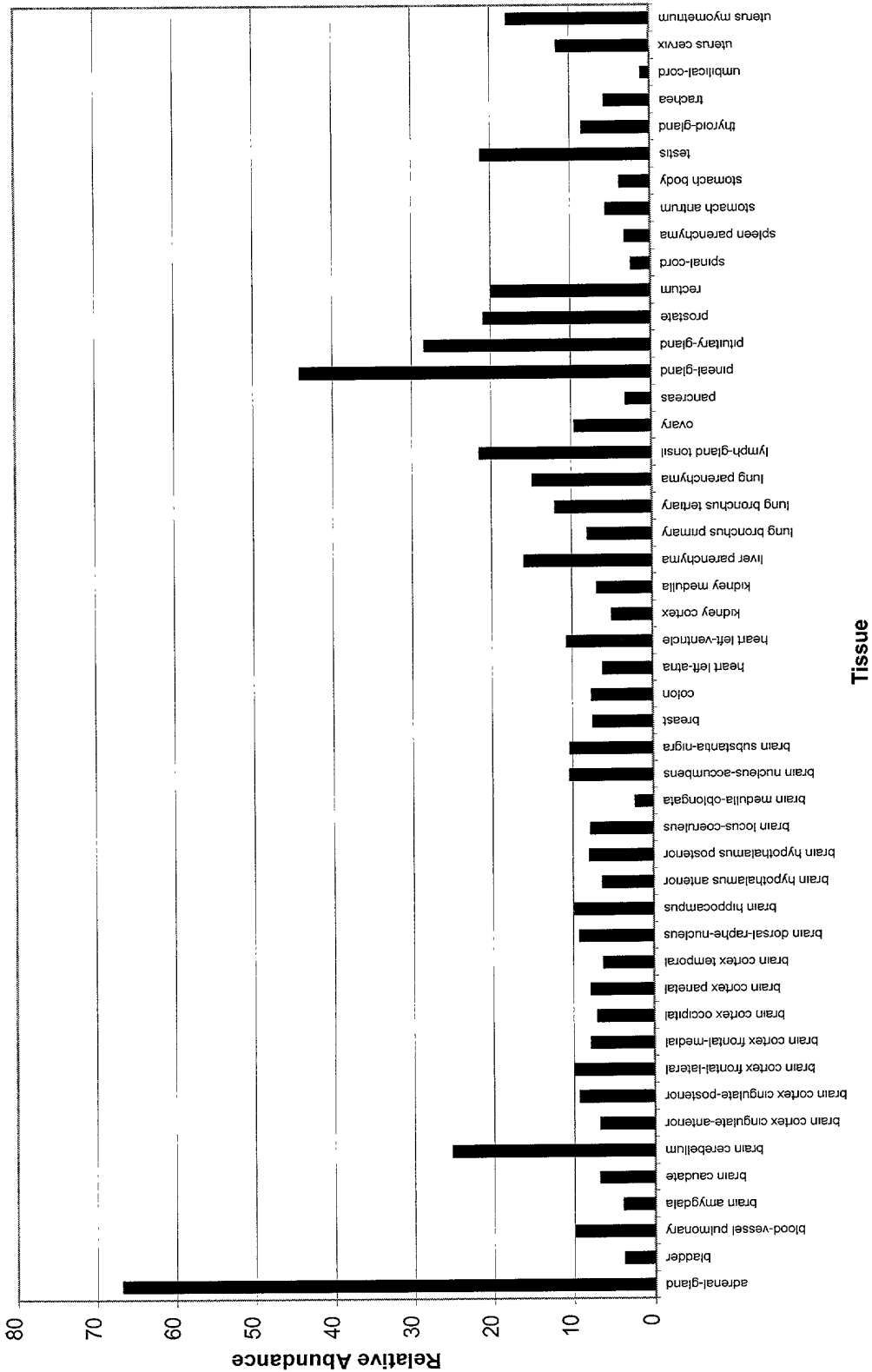


Figure 36

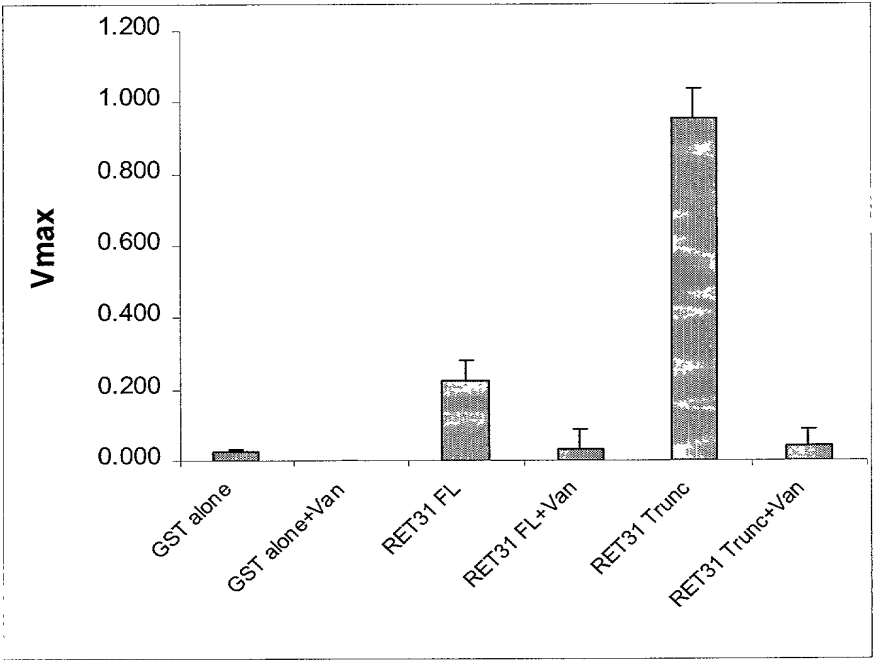


Figure 37

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                                10          20          30
pdblmkp      ASFPVEILPFLYLGC AKDSTNLDVLEEFGIKYI
              : : : : : : : : : : : : : : : : : :
BMY_HPP5     SRCFPGLCEGKSTLVPTCISQPCLPVANIGPTRILPNLYLGC QRDVLNKLMOQNGIGYV
              130          140          150          160          170          180

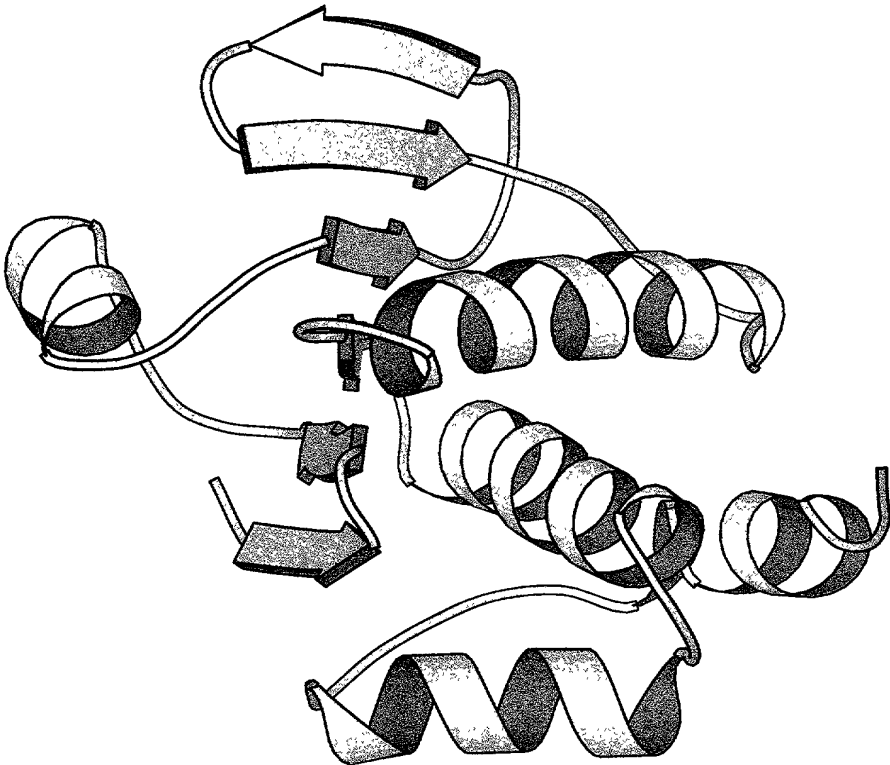
              40          50          60          70          80          90
pdblmkp      LNVTPNLPNLFENAGEFKYKQIPISDHWSQNLSQFFPEAISFIDEARGKNCGLVIVHSLAG
              : : . . : : . : . : . : . : . : . : . : : : : : : : : : : : : : : : : : : :
BMY_HPP5     LNASNTCPKP-DFIPESHFLRVPVND SFCEKILPWLDKSVDFIEKAKASNGCVLIVHCLAG
              190          200          210          220          230          240

              100          110          120          130          140
pdblmkp      ISRSVTVTVAYLMQKLNLSMNDAYDIVKMKKSNISPENFFMGQLDFERTL
              : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
BMY_HPP5     ISRSATIAIAYIMKRMDMSLDEAYRFVKEKRPTISPENFFLGQLLAYEKKIKNQTGASGP
              250          260          270          280          290          300

BMY_HPP5     KSKLKLPLEKPNEPVPVAVSEGGQKSETPLSPPCADSATSEAAGQRPVHPASVPSVPSVQ
              310          320          330          340          350          360

```

Figure 38



HPP5 Homology Model

Figure 39

